

XX (RIGE-) RIGEL PHARM INC.
PA

PI Luo Y, Huang BCB, Shen M, Yu PW;

DR WPI; 2000-205547/18.

DR P-PSDB; MAY45042.

PT Novel apoptotic proteins Apopt1, Apopt2 and Apopt3 and recombinant nucleic acids encoding them for use in screening modulators which is useful for PT diagnosis and treatment of diseases *

PS Claim 2; Flg 5; 64pp; English.

CC The patent discloses the use of novel apoptotic proteins and related
CC molecules involved in apoptosis modulation. Expression vectors
CC comprising the Apop DNA can be used to transform host cells. Apop DNA
CC can be administered as DNA vaccines. Apop proteins are used to make
CC polyclonal and monoclonal antibodies for use in immunotherapy. The
CC proteins are useful in treating apoptosis-mediated disorders including
CC cancer, autoimmune disorders, sustained viral infection, inappropriate
CC cell loss and degenerative disorders. Drug candidates that affect Apop
CC bioactivity are identified by screening. The present sequence encodes
CC Apop protein. This was identified using RIP (receptor-interacting
CC protein) as the bait protein employing the yeast two-hybrid screening
CC system. Human Apop is expressed in heart, liver, pancreas, placenta,
CC and lung. Overexpression of Apop inhibits TNF (tumour necrosis factor),
CC alpha-induced caspase activation without affecting TNFalpha-induced
CC NFkappa B activation.

50 Sequence 1557 BP; 397 A; 424 C; 446 G; 290 T; 0 other;

Query Match	100.0%	Score 1557;	DB 21;	Length 1557;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1557; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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Oy	61	ctggagagaaacaaagagatctcgttcggacaaagcgggttcctggacaagtgtctccggcgccacaacat	120
Db	61	ctggagagaaacaaagagatctcgttcggacaaagcgggttcctggacaagtgtctccggcgccacaacat	120
Oy	121	agagaaagtgtgggctctagctatctgtgcggtctcaaaatctgtaaaactctgaaagcgagatactcagggag	180
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Db	481	tctgtgcctgttcaaatcttcaaggaggtctcaaaagctcaaaagctcaaaagctcgggggtatgaccaggg	540

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OY	144.1	ccctctcgggcagaaaggagagggggtctctgacagaccccccacacagatgaggttctgcgaagaagagccct	1500
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RESULT	2
AAA47702	
ID	AAA47702 standard; cDNA; 1557 BP.
XX	

AC	AAA47702:
XX	
DT	08-NOV-2000 (first entry)
XX	
DE	Kinase of death (KOD) CDS.
XX	
KV	KOD; kinase of death; programmed cell death; apoptosis; cancer; autoimmune disease; stroke; Alzheimer's disease; identification; ds.
XX	
OS	Homo sapiens.
XX	
FM	Key
FT	Location/Qualifiers
FT	1..1557
FT	1-tag ^a
FT	/product- Kinase of death
XX	
PN	US6096539-A.
XX	
PD	01-AUG-2000.
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DR	WPI: 2000-523872/47.
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DR	P-PSDB: AAB01524.
XX	
PT	New nucleic acids encoding a protein activator of apoptosis for preventing, diagnosing and treating pathophysiological disorders related to apoptosis
XX	
PT	
XX	
PS	Claim 3; Columns 31-32; 32pp; English.
XX	
CC	The kinase of death (KOD) polypeptide is integral to the activation process of cellular apoptosis (programmed cell death). Apoptosis is needed to orchestrate biological maintenance of an organism during development as well as to preserve the normal function and fitness of tissues during a normal life span. Physiological conditions which result from aberrant apoptosis may be dire. Cancer and autoimmune disease may result when there is too little apoptosis as well as severe stroke damage or the neurodegeneration of Alzheimer's disease when there is too much apoptosis. The KOD polypeptide is useful for studying pathophysiological disorders related to apoptosis as well as for identifying compounds that modulate biological and/or pharmacological activity of the native mediator of apoptosis.
XX	
XX	Sequence 1557 BP; 395 A; 422 C; 448 G; 291 T; 1 other;

Query Match	99.5%	Score 1548.6;	DB 21;	Length 1557;
Best Local Similarity	99.6%	Pred. NO. 0;		
Matches 1551;	Conservative 1;	Mismatches 5;	Indels 0;	Gaps 0

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XX 19-NOV-2001 (first entry)
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De Human kinase of death (KOD) coding region.
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XX Human protein activator; apoptosis; kinase of death; KOD; therapy;
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US6267956-B1.
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PR 10-JUN-1999; 99US-0329418.
XX (ZENEC) ZENEC LTD.
XX Gomes BC, Kasof GM, Prosser JC;
XX WPI; 2001-535022/59.
XX P-PsDB: AAE09430.
XX
XX New human protein activator protein, useful for treating dysfunctional.
XX apoptosis conditions and in screening assays to identify agonists which
XX agonize or mimic biological and/or pharmacological activity -
XX
XX Disclousure: Column 31-32; 31pp; English.
XX
XX The invention relates to human protein activator of apoptosis and
XX methods to identify compounds that modulate the biological and/or
XX pharmacological activity of the activator and hence regulate
XX apoptosis. The nucleic acid and amino acid sequences of the kinase
XX of death (KOD) are useful for identifying compounds that modulate
XX the biological and/or pharmacological activity of a native mediator
XX of apoptosis, for treating dysfunctional apoptosis conditions, in
XX screening assays to identify agonists which agonize or mimic
XX biological and/or pharmacological activity, induce production of or
XX prolong the biological half-life of the molecule in vivo or in vitro.
XX The present DNA sequence is the coding region of human KOD protein
XX activator of apoptosis.
SQ Sequence 1557 BP; 395 A; 422 C; 448 G; 291 T; 1 other:

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Query Match 99.5%; Score 1548.6; DB 22; Length 1557;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1551; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Oy	1201	acctcaactcttcagaataaccagaatgcccagacccctaccctcaactggaatacacaagaactcttga	1260
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Db	1261	ccccgaggggaatccaaaggggctcgaagaagacaaagagcatalgaaactgtgtctcgaagaccggag	1320
Oy	1321	ccaaatcccaagtaacagagggcagccgcctcgttaacataatacaactctctcttgagtgatgca	1380
Db	1321	ccaaatcccaagtaacagagggcagccgcctcgttaacataatacaactctctcttgagtgatgca	1380
Oy	1381	ggagacaacaactactctgaactatgacaaagacgaactgcctctgcacacatgagggcttgaca	1440
Db	1381	ggagacaacaactactctgaactatgacaaagacgaactgcctctgcacacatgagggcttgaca	1440
Oy	1441	ccctctggcgaagggagggagggctctgcagaccccccacacagataggtctgcgaagaagggcct	1500
Db	1441	ccctctggcgaagggagggagggctctgcagaccccccacacagataggtctgcgaagaagggcct	1500
Oy	1501	aaagatccctggagagccttgagagagagcccaacaggggttgatatactatagcgggaataaa	1557
Db	1501	aaagatccctggagagccttgagagagagcccaacaggggttgatatactatagcgggaataaa	1557
RESULT 4			
AAK94599	ID	AAK94599 standard; cDNA; 1871 BP.	
AAK94599			
AAK94599			
06-NOV-2001	(first entry)		
Human full-length cDNA; SEQ ID NO: 3541.			
Human full-length cDNA; cDNA synthesis; oligo-capping; aa.			
Homo sapiens.			
EP1130094-A2.			
05-SEP-2001.			
07-JUL-2000; 2000EP-0114089.			
08-JUL-1999; 99JP-0194486.			
11-JAN-2000; 2000JP-0118774.			
02-MAY-2000; 2000JP-0183765.			
(HELI-) HELIX RES INST.			
Oka T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,			
Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;			
WPI; 2001-524255/58.			
P-PSDB; AAM93664.			
830 Primers useful for synthesizing full length cDNA clones and their			
use in genetic manipulation -			
Claim 8: SEQ ID NO 3541: 1380bp + sequence listing; English.			

XX	Query Match	98.8%	Score 1538	DB 22	Length 1871
CC	Best local similarity	99.6%	Ped. No. 0		
CC	Matches 1552	Conservative 0	Mismatches 5	Indels 1	Gaps 1
CC	1	ATCTGTCGTCAAGATTATAGCCAGCAGCTGCGCCGCCGCCCTCTGGTGTGCTCATCGAGGAA	60		
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CC	61	CTGTGGAAGCCAGGAGCGCTCGCTCGGCAAGAGCGGAGTTCGGACAAATGTCACGGGCGGACAT	120		
CC	225	CTGGAGAACCAAGAGAGCGCTCGGCAAGAGCGGAGTTCGGACAAATGTCACGGGCGGACAT	284		
CC	121	AGGAAATGTGGGTCTCAAGATGTGTGCTGTCAAGATCTGAAACTCGAAGCGATCATCCAGGAG	180		
CC	285	AGGAAATGTGGGTCTCAAGATGTGTGCTGTCAAGATCTGAAACTCGAAGCGATCATCCAGGAG	344		
CC	181	GTCAAGAGCCATGAGCAAGATCTCTGAGTCAACGAGATCTGTCTGCGCCCAAGAGGGTCTACAG	240		
CC	345	GTCAAGAGCCATGAGCAAGATCTCTGAGTCAACGAGATCTGTCTGCGCCCAAGAGGGTCTACAG	404		
CC	241	AAGGTGAATCTGGGCGCCAGAAATCTCCCAAGCGGAGTCTGTGTGATCTAAATCTCATGTGAGAGACGC	300		
CC	405	AAGGTGAATCTGGGCGCCAGAAATCTCCCAAGCGGAGTCTGTGTGATCTAAATCTCATGTGAGAGACGC	464		
CC	301	TCCCTGTCTGGGTGTGTCTGTCAAGTCCCAAGTGTCTCCAGTGTCTCGGCTCTCTTGTGCGCTGT	360		
CC	465	TCCCTGTCTGGGTGTGTCTGTCAAGTCCCAAGTGTCTCCAGTGTCTCGGCTCTCTTGTGCGCTGT	524		
CC	361	CTGAAAGAGAGTGTGTCTGTGTGATGTCTTACCTCTGTGACAGCAAGAACCCGGTGTCTCTGAC	420		
CC	525	CTGAAAGAGAGTGTGTCTGTGTGATGTCTTACCTCTGTGACAGCAAGAACCCGGTGTCTCTGAC	584		
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CC	481	TTTGGCTGTCTCAACATCTCCAGGGAGAGCTCAACAGTCCAGAGGACAGGTCTCCGGGGAGCCAGG	540		
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CC	661	GGATTTCCCAACCGAACAATACATCTCTGTGATGAAGAGCAATGTGCAACAGGAGAGAACCGGCT	720		
CC	825	GGATTTCCCAACCGAACAATACATCTCTGTGATGAAGAGCAATGTGCAACAGGAGAGAACCGGCT	884		
CC	721	TCAATGTCTGTAGCTGTGCCCAAGTCCGGGCTCAAGATCTCCGGTCTAAGAGGACTCAAGAG	780		
CC	885	TCAATGTCTGTAGCTGTGCCCAAGTCCGGGCTCAAGATCTCCGGTCTAAGAGGACTCAAGAG	944		


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Db 241 cctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 300
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Db 1021 tcttaaaaaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1080
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Db 1141 cttaaaacttcaagaaacagagatgcccagccctacactcaacttggaacacacagctcctgagac 1200
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RESULT 8
AAAT5675
ID AAAT5675 standard; DNA: 2140 BP.
XX
AC AAAT5675;
XX
DT 22-JAN-2001 (first entry)
XX
DB DNA encoding a human regulator of intracellular phosphorylation.
XX
NM Human; intracellular phosphorylation regulator; RHP; stroke; myeloma;
NM neurological disorder; Parkinson's disease; demyelinating disease;
NM meningitis; developmental disorder; neuromuscular disorder; cancer;
NM myasthenia gravis; cell proliferative disorder; actinic keratosis;
NM arteriosclerosis; atherosclerosis; leukemia; melanoma; bronchitis;
NM autoimmune disorder; inflammatory disorder; Addison's disease;
NM acquired immunodeficiency disease; allergy; diabetes mellitus;
NM rheumatoid arthritis; microbial infection; trauma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 395..1852
FT /tag="a
FT /product="regulator of intracellular phosphorylation"
XX
MO20005332-A2.
XX
PD 21-SEP-2000.
XX
PE 17-MAR-2000; 2000NO-US07277.
XX
PR 18-MAR-1999; 9905-0125593.
PR 20-MAR-1999; 9905-0135049.
PR 09-JUL-1999; 9905-0143188.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Tang YT, Yue H, Hillman JL, Baughn MR, Azimzal Y;
PI Lu DM, Au-Young J;
XX
DR MPI: 2000-602121/57.
XX
P-PSDB: AAB16658.
XX
PT Novel human intracellular phosphorylation regulator polypeptides and
PT polynucleotides for diagnosis, prevention and treatment of

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AA30546
ID AAF30546 standard; cDNA; 1437 BP.
XX
XX AAF30546;
XX
DT 29-MAY-2001 (first entry)
XX
XX Rat RIP-3-like death-associated kinase (R3DAK) cDNA.
XX
XX RIP-3-like death-associated kinase; R3DAK; rat; antibacterial;
XX virucide; protozoacide; cardiant; antiinflammatory; vasotropic;
XX antidiabetic; antitumour; analgesic; immunosuppressive;
XX antihypertoid; antilucer; nephrotropic; cytosaric; nocotropic;
XX anticonvulsant; hepatotropic; antiallergic; antigenic;
XX dermatological; osteotropic; antiallergic; uropathic;
XX ophthalmological; antiparkinsonian; antipsoriatic; neuroprotective;
XX pulmonary; hormonal; apoptosis; gene therapy; vaccine; 88.
XX
XX Rattus sp.
XX
XX WO200119990-A1.
XX
XX 22-MAR-2001.
XX
XX 15-SEP-2000; 2000MO-US25201.
XX
XX 17-SEP-1999; 99US-0154422.
XX
XX (IMMUNEX CORP.
XX
XX Vixra CD, Bird TA:
XX
XX WPI: 2001-244803/25.
XX
XX P-PSDB: AAB20345.
XX
XX New isolated RIP-3-like death-associated kinase polypeptide for
XX treating multiple sclerosis, Parkinson's disease, Sjogren's disease,
XX infections, tumours, cardiovascular and lymphoproliferative disorders
XX
XX Claim 5: Page 56-57; 63pp; English.
XX
XX The present sequence is that of the coding region of cDNA encoding
XX rat RIP-3-like death-associated kinase (R3DAK, see AAB20345), a
XX member of the RIP3 family, which is known to be involved in
XX apoptosis. The cDNA was obtained from a rat dermal papilla cell
XX library. The invention provides R3DAK polypeptides and a
XX polynucleotide, expression vectors, recombinant host cells, and
XX methods of producing a recombinant R3DAK polypeptide, as well as
XX antibodies, a method of designing an R3DAK inhibitor on the basis
XX of the 3-dimensional structure of a R3DAK polypeptide, a method of
XX identifying compounds that alter R3DAK kinase activity, and for
XX using such compounds. R3DAK, its fragments, variants, antagonists,
XX agonists, antibodies and binding partners are useful for treating:
XX bacterial, viral or protozoal infections; cardiovascular disorders such
XX as myocardial infarction, heart failure, or vasculitis; solid tumours;
XX chronic pain; endocrine system disorders such as diabetes;
XX hypothyroidism and thyroiditis, including Hashimoto's thyroiditis;
XX gastrointestinal diseases such as Crohn's disease and ulcers;
XX genitourinary system disorders such as glomerulonephritis; haematologic
XX and oncologic disorders such as cancer; lymphoproliferative disorders
XX such as Hodgkin's disease; hereditary conditions such as Gaucher's and
XX Huntington's disease; liver disorders such as hepatitis; non-arthritic
XX medical conditions of the bones and joints; pulmonary disorders such as
XX cystic fibrosis; allergies; rheumatic disorders such as systemic lupus
XX erythematosus, gout, osteoarthritis, Reiter's disease;
XX graft-versus-host disease; female reproductive system disorders; and
XX diseases such as multiple sclerosis, Parkinson's disease, Sjogren's
XX disease. R3DAK is useful for effecting bodily characteristics,
XX biohythme or cardiac cycles or rhythms; effecting the fertility of
XX male or female subjects; effecting the metabolism, catabolism
XX anabolism, processing, utilization, storage or elimination of dietary
XX fat, lipid, polypeptide, carbohydrates, vitamins, minerals, cofactors
XX or other nutritional factors or component(s); effecting behavioural

CC characteristics; providing analgesic effects or other pain reducing
CC effects; promoting differentiation and growth of embryonic stem cells
CC in lineages other than haematopoietic lineages; hormonal or endocrine
CC activity; treatment of hyperproliferative disorders;
CC immunoglobulin-like activity; and the ability to act as an antigen in a
CC vaccine composition. Nucleic acids encoding R3DAK are useful for
CC diagnostic purposes, for expressing recombinant polypeptide for
CC analysis, characterization or therapeutic use, as markers for tissues
CC in which the corresponding polypeptide is preferentially expressed,
CC to compare with endogenous DNA sequences in patients to identify
CC potential genetic disorders; as an antigen to raise anti-DNA
CC antibodies or elicit another immune response; and for gene therapy.
XX
XX Sequence 1437 BP; 368 A; 359 C; 399 G; 311 T; 0 other:
SO
Query Match 43.3%; Score 673.6; DB 22; Length 1437;
Best Local Similarity 69.4%; Pred. No. 9.5e-175;
Matches 1024; Conservative 0; Mismatches 404; Indels 48; Gaps 6;
OY 1 ATGCTGCTCAAGTATGAGCCAGCGTCCCGC---CCCTGCTGCTCAAG 57
DB 1 ATGCTGCTCAAGTATGAGTATGCTGCTCAAGTATGCTGCTGCTGCTGAA 60
OY 58 GAATGAGAGAGCAAGAGAGTCTGCGCAAGAGGCTGAGAGAGTCCGAGCA 117
DB 61 GAATGAGAGAGCAAGAGAGTCTGCGCAAGAGGCTGAGAGAGTCCGAGCA 120
OY 118 CATAAGAGTGGGCTGAGAGTCTGCGCAAGAGTCAAGTCAAGAGAGTCAAG 177
DB 121 CACAAGAGTGGAGAGTCTGAGTCAAGAGTCAAGTCAAGAGAGTCAAGAG 180
OY 178 GAGTCAAGAGTCAAGAGTCAAGTCAAGAGTCAAGTCAAGTCAAGAGAGTCA 237
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OY 298 GGTCTCTGCTGAGTCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 357
DB 301 GGTCTCTGCTGAGTCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 360
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OY 418 CACGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 477
DB 421 CACGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 480
OY 478 GATTTGCTGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 531
DB 481 GATTTGCTGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 540
OY 532 GAGCAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 591
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OY 592 GCTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 651
DB 598 GCTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 657
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DB 658 AGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 717
OY 712 AAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 771
DB 718 AAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 777
OY 772 CTGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 831


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Db 778 ctgaaggggttaattacgcatctgtgagcttcgagccctaaagacagccatctctcca 837
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Db 1342 gtgcaagattgacacacacacatgactgactgacacacagacagacagacagacagag 1401
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Oy 1432 ggtctgcacactcggcgaagagagagagagagagagagagagagagagagagagag 1467
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ID AKS7466 standard; cDNA; 939 BP.
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AC AKS7466;
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DT 06-NOV-2001 (first entry)
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DE Human Immune/Haematopoietic antigen encoding cDNA SEQ ID NO:2526.
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KW Human; Immune; haematopoietic; Immune/Haematopoietic antigen; cancer;
KN Cytotoxic; gene therapy; vaccine; metastasis; ss.
OS
XX Homo sapiens.
XX
PM WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US01354.
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PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 02-MAR-2000; 2000US-0186350.
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PR 02-OCT-2000; 2000US-0237040.
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PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
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 PR 01-DEC-2000; 2000US-0250160.
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 PR 08-DEC-2000; 2000US-0251889.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR MPI: 2001-465460/50.
 DR P-PSDB; MA017293.
 XX
 PT Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders -
 XX
 PS Claim 1; SEQ ID No 245; 880bp; English.
 XX
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). MAS2676-MAS27850 represent novel signal transduction
 CC pathway protein coding sequences and PCR primers of the invention.
 CC
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 Query Match 40.4%; Score 629; DB 22; Length 960;
 Best Local Similarity 95.8%; Pred. No. 1.4e-162;
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 Db 225 ctggaagaccagagagctcgtcgcgaagcgggttcgcagacgtgtccggcgacacat 284
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 Db 455 tccctctggagctgtctgaatctccagctgcctcggcctccttcgtccgctc 524
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 OY 718 ccttccttgccgagctgcgcc--aagcgggctcgaatcccggtta--gaagagact 773
 Db 880 -ccttccttgccgagctgcgcccaagcgggctcgtgaatnccgcttaanaagactt 938
 OY 774 gaagagctaatatgc 787
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 AC AAK92320;
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 DT 06-NOV-2001 (first entry)
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 DE Human cDNA 5'-end sequence, SEQ ID NO: 780.
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 KM Human: full length cDNA; cDNA synthesis; oligo-capping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1130094-A2.
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 PD 05-SEP-2001.
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 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Iahli S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuka T, Koga H;
 XX
 DR MPI: 2001-524255/58.
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OY 481 ttggcctgcacattccaggga 504
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AC
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DT
XX Human Immune/Haematopoietic antigen genomic sequence SEQ ID NO:25225.
DE
XX Human; Immune; haematopoietic; Immune/Haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
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OS Homo sapiens.
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XX MO200157182-A2.
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Oy	541	ggacaacctg.9gcctacttggccccagaactgttttgttaacgtaaacggagagcgctccc	599	
Db	683	GCCACCCTGTGGCTACTTGCGCCCCCACAACACTGTTGTATACGTAAACCGGAAGGCTCTCAC	742	
Oy	600	aagccagtgaagcttacagctcttggagatcctaattgtgggcagtagtctcttggaaaagaat	659	
Db	743	AG-CAGTGACGCTCACAGCTTCGGGATCCTAATGTGGCAGTAGCTCTGTGGAAGAAGAT	801	
Oy	660	tgaattgccaacagcaaccatactactgtgtlgaagaaagcagltgtcaaacagcagaagccggc	719	
Db	802	TGACTGTCCCAA-CCAAACCATCATCTGGTGTGCAAAACACTGTGCACACGACGAAACCGG-C	859	
Oy	720	ttcatctgtcagctgtgcccccaagccgg	746	
Db	860	TTTCCTGCTGACTGACTGCCCAAGCCGGG	886	
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ACCESSION	B1819557	mRNA sequence.		
VERSION	B1819557	EST.		
KEYWORDS	B1819557.1 GI:15931107			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryote; Metazoa; Chordata; Carnivora; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Rutheria; Primates; Canarrhini; Homnidae; Homo.			
TITLE	I (passed 1 to 1026)			
JOURNAL	NIH-MGC http://mgs.mcl.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: egsab@remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: ELAM1443 row: k column: 19 High quality sequence spot: 860. Location/Qualifiers .1..1026 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="5177994" /clone_lib="NIH_MGC_115" /lab_host="DH10B" /note="Organ: Pooled brain, lung, testis; Vector: pcmv-SPORE6; Site_1: NCI; Site_2: ECoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 73-87; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (ECoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."			
FEATURES	Source			
BASE COUNT	230 a	298 g	198 t	2 others
ORIGIN	298 c			

Matches	793	Conservative	0	Mismatches	37	Indels	12	Gaps	9
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Db	148	ATGTCGTCGCTCAAGTATTATGCCCCAGCCGATGCCCCCCCTTGCGGTGCTCATCGAGAA	207						
QY	61	ctgagaaacacgaagagctcgtccgcgaagaacggtgtcgtgcacagtgttcgcggcgcaacat	120						
Db	208	CTGAGAACCAAGAGAGCTGCTCGGCAAAAGCGGGTTCGGCACAGTGTCTCCGGGCGCAACAT	267						
QY	121	aggaagatgaggagctacagatgttgccggtcgaagatgcttaaacctgaaagcgatataccagagag	180						
Db	268	AGGAAGTGGGGGCTACATGTGGCGGTCAAGATCGTAACTGAAAGGCGGATATCCANAGAG	327						
QY	181	gtcaagagcatalgcaagatctggaataagaaltcgtgtgtgcctagaagagggtatctcag	240						
Db	328	GTCAGAGCCATGCGCAAGTGTGATTAACGAAATTCGTGCTGCCCTCAGAAAGGGTTATCGAG	387						
QY	241	aaggtctgaacctgaggaacaaagatcccaagccggctcgtgtgacttaaatcattgagaaacgag	300						
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QY	361	ctgaagaagtggtgtgtctgtggaatgttttaacctgcaagcaagaaacccggtgtctctgcac	420						
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Db	866	CGGCGCTTTCATATGTCTGAAGCTGCGCCCAACCCGGGCTGAGATTCCTCGGAGATTAAAGCC	925						
QY	772	ctgaagagagctaatgtcagctc -tgtctgagagcagtgagcccaagagacagacc	822						
Db	926	TGCAAGAGCGCTAATTGCGGCTGTGGGGGACACAGTAGACCCAGAAAGCCCTC	977						
RESULT	4								
LOCUS	B1823411								
DEFINITION	B1823411	922 bp	mrna	linear	EST	04-OCT-2001			
ACCESSION	603041149P1	NH_MGC_115	Homo sapiens	cDNA clone IMAGE:5181972	5'				
VERSION	B1823411								
KEYWORDS	B1823411.1	GI:15934961							
SOURCE	EST								
ORGANISM	human.								
	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1 (bases 1 to 922)								
AUTHORS	NH-MGC	http://mgc.ncl.nih.gov/.							

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at:
http://image.llnl.gov
Plate: LLM11454 Row: a Column: 13
High quality sequence start: 2
High quality sequence stop: 785.
Location/Qualifiers

FEATURES
source 1..922
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5181972"
/clone_id="NTH_MGC_115"
/abd_host="DH10B"
/note="Origin: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (In vitro). Research Genetics tracking code 021. Note: this is a NTH_MGC Library."

BASE COUNT 206 a 269 c 270 g 177 t
ORIGIN

Query Match 39.6%; Score 615.8; DB 10; Length 922;
Best Local Similarity 95.1%; Pred. No. 7.6e-145;
Matches 712; Conservative 0; Mismatches 27; Indels 10; Gaps 7;

1 atgtctgctcaagttatgagccagtgagccgccccttggtgctcattcagagga 60
|||||
Db 173 atgtctgctcaagttatgagccagtgagccgccccttggtgctcattcagagga 232
61 ctggagaacccagagagctctgagcaagagcggttcgagcagtgctcgggagcaacat 120
|||||
Db 233 ctggagaacccagagagctctgagcaagagcggttcgagcagtgctcgggagcaacat 292
121 aggaagctggagctacgagctggcggttcagagctcgttaactcgaagcgatataccagagag 180
|||||
Db 293 aggaagctggagctacgagctggcggttcagagctcgttaactcgaagcgatataccagagag 352
181 gtcaagagcagtgagcagagcttgagtaagaatctgttctgagcctagaagaaggttataccag 240
|||||
Db 353 gtcaagagcagtgagcagagcttgagtaagaatctgttctgagcctagaagaaggttataccag 412
241 aaggtgaactggagcagagatcccaagcgggtctgttgatataatcattatgagaagagc 300
|||||
Db 413 aaggtgaactggagcagagatcccaagcgggtctgttgatataatcattatgagaagagc 472
301 tccctctcggagctgagcagctcagagctcagcctcggcctcggcctccttgcagcctg 360
|||||
Db 473 tccctctcggagctgagcagctcagagctcagcctcggcctcggcctccttgcagcctg 532
361 ctgaagaagaagtggtgcttgagtggttcttaactgacagacaggaaccgggtgctcctcagc 420
|||||
Db 533 ctgaagaagaagtggtgcttgagtggttcttaactgacagacaggaaccgggtgctcctcagc 592
421 cggagacccataagccataccagctcctcgcgagaccagagctgacagctcagagctgagat 480
|||||
Db 593 cggagacccataagccataccagctcctcgcgagaccagagctgacagctcagagctgagat 652
481 ttctggcctctcagacattcagagagagctcagagctcagagagcagaggtc-cggggaagcagag 539
|||||

Db 653 ttmgcctctgctcagctatttcagagagctcagacagcagcagcctcccgagagccagc 712
Qy 540 gggcaccctgggctacttgagccagagacgtttgttaacgttaa--ccgaaagagcctcc 597
|||||
Db 713 gggcaccctgggctacttgagccagagacgtttgttaacgttaa--ccgaaagagcctcc 772
Qy 598 acagcagtgagc-ctacagctt-cggagacctaag-tyggcagctgcttgctggaaga 654
|||||
Db 773 acagcagtgagc-ctacagctt-cggagacctaag-tyggcagctgcttgctggaaga 832
Qy 655 gaa---gttagttgcacacgaaacataactggtgtaagagcagtgtagcaagagcag 711
|||||
Db 833 gaaacgttagttgcacacgaaacataactggtgtaagagcagtgtagcaagagcag 892
Qy 712 aacc-ggcttcattgctgagctgcccc 739
|||||
Db 893 aaccggccttgcattgctgagctgcccc 921

RESULT 5
LOCUS AN959157 630 bp mRNA linear EST 01-JUN-2000
DEFINITION EST371227 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AN959157
VERSION AN959157.1 GI:8148841
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 630)
Hogde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeaman,T.J. and
Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnqu@tigr.org
Plate: 130
Seq primer: Reverse.
Location/Qualifiers

FEATURES
source 1..630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="MAGE resequences, MAGE"
/note="Vector: pBluescriptKm"

BASE COUNT 180 a 170 c 164 g 116 t
ORIGIN

Query Match 38.6%; Score 600.4; DB 9; Length 630;
Best Local Similarity 98.1%; Pred. No. 3e-141;
Matches 618; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

849 tgatgaagttctcagagatggtgagaaacatatagaatgctgcttcccaagataaagga 908
|||||
Db 1 tgatgaagttctcagagatggtgagaaacatatagaatgctgcttcccaagataaagga 60
Qy 909 ttctctctcagctcagaagagagagcaatagagatttctatccagagagctagagcagag 968
|||||
Db 61 ttctctctcagctcagaagagagagcaatagagatttctatccagagagctagagcagag 120
Qy 969 aggagacaaatgagatgagctttagagagaacataagaacacagcactctcgtatgagat 1028
|||||
Db 121 aggagacaaatgagatgagctttagagagaacataagaacacagcactctcgtatgagat 180
Qy 1029 catgttctcagagtggtcagaacacatgactatgagagagcctcccaagctctgttcttaa 1088
|||||

[illegible][illegible]


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OY 395 agagcagaagccggtgctcctcgcacgagccctcaagccatcccaagctcctgcgagac 454
DB 602 ACAGCTTGAACCTCTCGCTCTCTGACACCGGACCTCAAGCCTCTCAATCTCTGATC 661
OY 455 cagagctgcagctcaagctgcagagatttcgctcctcacaattcagggagctcagct 514
DB 662 CAGAGCTCCACGCGCAAGATGATTTGGCTGCTCCATTCACGATTCAGGAGCTCCACT 721
OY 515 cagagcagaagctcagc-----gagcagaagcagcagctcagctcagctcagcagc 563
DB 722 CAGGCTCAGGATCAGATCAGATCAGAGGACTCTGGGCGGACCTTACGCTACTGGACCC 781
OY 564 agagctgcttgcagctcaagcagagcctcagcagcagctcagctcagctcagctcag 623
DB 782 AGAGCTGATTTATTTGATGCT-CACCTAAGGCTCTTAAAGCGAGTATCTTACAGCTTGG 840
OY 624 gaccccaatgtgagcagctcgtcctgcagagagagcttgcagctcagcagcagcagcact 683
DB 841 GATCTCTGCTGCGGAGCTGCTGCTGCGGAGAGAGCTGATGCTGATACAGAGCTTCACT 900
OY 684 cgtgtcagaagcagctgcagcagcagcagcagcagcagcagcagcagcagcagcagc 743
DB 901 AATCCGGAAGAAAGTGTGTGACAGGAGAGTGTGTCTCACTGACAGGCTGCTTCA--- 957
OY 744 cgggctgagctcagcagctcagagagcagcagcagcagcagcagcagcagcagcag 803
DB 958 --GTAACCTGAAACCCGCGCTTGA--AACTGAAGAGTTATGATCTGCTGCG--CTTC 1012
OY 804 tgaagcagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 863
DB 1013 CCAAGCTCGAAGAAAGGCTCTCTTCCAGAGCTGCGAAGCAAGAAACCAATTAATTACAA 1072
OY 864 gtagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 923
DB 1073 TCTGCTAAAGGAGCAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1132
OY 924 cagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 983
DB 1133 CAGAAACAGCGGAGCAAACTGTCTGCGAGAGAGCAAGCAAGCAAGCAAGCAAGCAAG 1192
OY 984 tgccttgcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1043
DB 1193 TTTCCCGAGGAAAC-----CATGCTTCTTAAAT 1222
OY 1044 gctcaaacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1103
DB 1223 GCTGGACCGCTGCAATTGTGAGAGAACCTCTCGGACAGTTCCTGGAAATGATC----- 1276
OY 1104 taccagaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1163
DB 1277 -----TGAGAGCGCAAGCAGACATCATGTTGCGCTGCGCAGCAGCAGCAGCAGCAG 1330
OY 1164 ttcagagctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1223
DB 1331 TTTGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1390
OY 1224 gcccagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1283
DB 1391 ACCTGGGCGCAAGTCTTACTGAGAGACCTCTCGGACAGTTCCTGGAAATGATG 1450
OY 1284 gagaacagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1343
DB 1451 AAGACACGCGCAGCTCTTGGTATTCCTGAGACCC--ACCGAATCGAATGACAGGCGCAGC 1507
OY 1344 gctcgttgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1403
DB 1508 GCTCTCTGCTTTCACAACTGTTCTGAGATGAGATGAGGAGCTACAACTCTCTGTTAGC 1567
OY 1404 ggaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1454
DB 1568 ACCACCAAGAACTACTGCTCAAGTTGCGGCAAGTATGACCAAGCAAGTGTGCGCAGGG 1627

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```

OY 1455 gaggagctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1514
DB 1628 TAGGGCTGGAGC-CCTTCCAGAACTGACTTCAAGAAATCTGCAAGAGCTGAAAT 1686
OY 1515 cttg 1517
DB 1687 GTG 1689

RESULT 7
BFO01916/c 643 bp mRNA linear EST 06-OCT-2000
LOCUS 795610.X1 NCI-CGAP.CO16 Homo sapiens cDNA clone IMAGE:311226 3'
DEFINITION Similar to TR:097572 091572 RIP-Like KINASE. ; mRNA sequence.
ACCESSION BFO01916
VERSION BFO01916.1 GI:10702191
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 643)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN. send email to:
InfoImage.linn.gov
Seq primer: -40UP from Glbco
High quality sequence atop: 166.
FEATURES
source
location/Qualifiers
1..643
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3114226"
/clone_lib="NCI CGAP.CO16"
/tissue_type="Colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: Colon; Vector: p77TD-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP.CO16 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1057416-1061255 and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bomalido.
BASE COUNT 129 a 166 c 162 g 186 t
ORIGIN
Query Match 29.8%; Score 464; DB 10; Length 643;
Best Local Similarity 82.8%; Pred. No. 1.3e-106;
Matches 581; Conservative 0; Mismatches 35; Indels 86; Gaps 1;
OY 856 gtcttcagagctgtagaacaatgtagctgtctcagcagcagcagcagcagcagcagc 915
DB 643 GTCTTCAAGATGATGAGACTAAATCTCTGAGGCTTACACGCTAAAGATTTCTCTG 584
OY 916 tctcagctcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 975
DB 583 TATCATGTTAGCGAGCAGCAATAGAGATGTATTTCCACAGCAGCATCTAGCAGCGCA 524
OY 976 gaatgatgcttgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1015

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Db 523 GATTGATGCTCTAGAGATCCATAGTTAACAGACACTCTCTAATGATGTCATGCTT 464
Oy 1036 tctgagtgctaaacaaactgaatctagagagagcctcccaactctcttctctaaataatc 1095
Db 463 TCTGATGCTGTTAAACATCTGACATCTAGAGAGAGCTCCCACTGCTGTTCCATAATATGC 404
Oy 1096 cggagccttaccagagagagcagagagagagagagagagagagagagagagagagagag 1155
Db 403 CCGAGCCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 344
Oy 1136 ggcacatcttcagatctgagtgcacacactcccaagactccagagagacttaattcaga 1215
Db 343 GGCACATCTTACATGATGAGGCGCCCAACTCCCAAGACTCC----- 301
Oy 1216 aaccagatgcccagccttacttaacttgaaacacaaagtccttgagcccgaggagatcag 1275
Db 302 ----- 301
Oy 1276 gggagctgagagagagagagatgaactgctcctgagagaccgagagcgaatccaagtaca 1335
Db 302 -----AGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 250
Oy 1336 gggcagccgctcgttcaacatatacaactgctcggggtgcaagcttgagagagagagag 1395
Db 249 GGGGAGACCGCTCGTTAATATATACATGCTGCTGGGGTGCAGATTGAGAGACAACTAC 190
Oy 1396 ttgactatgagagagagagagagagagagagagagagagagagagagagagagagagag 1455
Db 189 TTGACTATGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 130
Oy 1456 agggagcttgagagagagagagagagagagagagagagagagagagagagagagagagag 1515
Db 129 AGGGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 70
Oy 1516 tggagcagagcagagagagagagagagagagagagagagagagagagagagagagagag 1557
Db 69 TGGAGCAGCGCCACAGCGCTTGCTATATCATACCGGAAATATA 28

RESULT 8
AL601137 758 bp mRNA linear EST 14-AUG-2001
LOCUS DKEZp31300939.1 313 (synonym: h1cc2) Homo sapiens cDNA clone
DEFINITION DKEZp31300939 5', mRNA sequence.
AL601137
ACCESSION AL601137.1 GI:15164643
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 758)
AUTHORS Duesterhoeft,A., Lauber,J., Meves,H.W., Gassenhuber,J. and Wiemann
,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Duesterhoeft A
MIPS
Am Klopferpitx 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann. Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 31 sequence available.
This clone (DKFZp31300939) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcencentrum, Heubenerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
location/Qualifiers
1. 758
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp31300939"

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BASE COUNT 167 a 231 c 211 g 145 t 4 others
ORIGIN
Query Match 29.8% Score 463.4; DB 9; Length 758;
Best Local Similarity 98.7%; Pred. No. 2.3e-106;
Matches 467; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy 1 atctgtgctcagatgatgagcagagagagagagagagagagagagagagagagagagagag 60
Db 192 ATCTGCTCGTCAAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 251
Oy 61 ctgagagacagagagagagagagagagagagagagagagagagagagagagagagagagag 120
Db 252 CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
Oy 121 aggaagtgaggctacgagctgagcagagagagagagagagagagagagagagagagagag 180
Db 312 AGGAAGTGAGGCTACGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
Oy 181 gtcagagcagagagagagagagagagagagagagagagagagagagagagagagagagag 240
Db 372 GTCAAGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
Oy 241 aaggtgaacttgagagagagagagagagagagagagagagagagagagagagagagagagag 300
Db 432 AAGGTGAATCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
Oy 301 tccctgtcgggagagagagagagagagagagagagagagagagagagagagagagagagag 360
Db 492 TCCCTGTGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
Oy 361 ctgaagaagatgagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
Db 552 CTGAAGAAGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
Oy 421 cggagcctcagagcagagagagagagagagagagagagagagagagagagagagagagag 473
Db 612 CGGAGCCTCAAGCCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 664

RESULT 9
B1833736 616 bp mRNA linear EST 04-OCT-2001
LOCUS B1833736 616 (bases 1 to 616)
DEFINITION B1833736 616 (bases 1 to 616) Homo sapiens cDNA clone IMAGE:3227291 5',
B1833736
ACCESSION B1833736
VERSION B1833736.1 GI:15945286
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 616)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: U96A1572 row: a column: 20
High quality sequence stop: 616.

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FEATURES
SOURCE

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FEATURES
SOURCE
Location/Qualifiers
1. 616
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5272291"
/clone_lib="NIH_MCC_120"
/lab_host="DH10B"
/lab="Organ: pooled pancreas and spleen; Vector:
pCVC-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV) site is destroyed upon cloning). Average insert
size 1.5 kb. Insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invtitrogen). Research Genetics
tracking code 023. Note: this is a NIH_MCC Library."
134 a 188 c 177 g 117 t

```

TITLE	,T., Waterston,R. and Wilson,R
JOURNAL	WashU-Merck EST Project 1997
COMMENT	Unpublished (1997)
	Contact: Wilson RK

TITLE 'T', Waterston, R. and Milson, R.
JOURNAL Mashu-Merck EST Project 1997
COMMENT Unpublished (1997)
Contact: Milson Rk
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@waterston.wustl.edu
This clone is available royalty-free through LNC; contact the
IMAGE Consortium (info@image.lnh.gov) for further information.
Insert Length: 829 Sd Error: 0.00
Seq primer: -26m3 rev2 ET from Amer sham.

FEATURES

BASE COUNT
ORIGIN

131 a 119 c 111 g 79 t

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/organism="Homo sapiens"  
/db_xref="GDB:5561280"  
/db_xref="taxon:9606"  
/clone="IMAGE:667313"  
/clone_1lb="Scares_NhMMPu.S1"  
/tissue_type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"  
/lab_host="DH10b"  
/note="Organ: mixed (see below); Vector: pT73D-Pac  
(Pharmacia); with a modified polylinker; site.1: Not i;  
site.2: Eco RI; Equal amounts of plasmid DNA from three  
normalised libraries (melanocyte 2NbM, pregnant uterus  
NBHPU, and fetal heart NBH19W) were mixed and as circles  
were made in vitro. FOLLOWING HAP purification this DNA  
was used as tracer in a subclonally hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3.1kbra5G6. The pools  
consisted of 1.M.A.G.B. Clones 260232-265223,  
340488-345379, and 484488-489479.
```

Query Match	27.3%	Score 425.8;	DB 9;	Length 440;
Best Local Similarity	99.3%;	Pred. NO. 5.6e-97;		
Matches 438; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1;

[illegible]

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	MEDLINE	COMMENT
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	BF359285	BC6-ET0081-100700-012-B10 ET0081 Homo sapiens cDNA, mRNA sequence.									
	BF359285.1	GI:11318461									
	human.										
	Homo sapiens										
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	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.										
	1 (bases 1 to 432)										
	Daa Neto,E.; Garcia Correa,R.; Vertovski-Almeida,S.; Britones,M.R.;										
	Nagai,M.A.; da Silva,M.Jr.; Zago,M.A.; Bordin,S.; Costa,F.F.;										
	Goldman,G.H.; Carvalho,A.F.; Matsumoto,A.; Bala,G.S.; Simpson,D.H.										
	Brunstein,A.; deoliveira,P.S.; Bucher,P.; Jongeneel,C.V.O'Hare										
	.M.J.; Soares,F.; Brentani,R.R.; Reis,L.F.; de Souza,S.J.; and										
	Simpson,A.J.										
	Shotgun sequencing of the human transcriptome with ORF expressed										
	sequence tags										
	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)										
	20202683										
	Contact: Simpson A.J.G.										
	Laboratory of Cancer Genetics										
	Ludwig Institute for Cancer Research										
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,										
	Brazil										
	Tel.: +55-11-2704922										
	Fax: +55-11-2707001										
	Email: asimpson@ludwig.org.br										
	This sequence was derived from the PAPESP/LICR Human Cancer Genome										
	project. This entry can be seen in the following URL:										
	(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-ET0081-100700-012-B10&t3=2000-07-10&t4=1)										
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	/clone_lib="ET0081"										
	/dev_stage="Adult"										
	/note="Organ: Lung tumor; Vector: puc18; Site:1: Smal;										
	Site:2: SmaI; A mini-library was made by cloning products										
	derived from ORESTES PCR (U.S. letters patent application										
	No. 196,716 - Ludwig Institute for Cancer Research)										
	Profiles into the pUC 18 vector. Reverse transcription of										
	tissue mRNA and cDNA amplification were performed under										
	low stringency conditions."										
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	Best Local Similarity	96.6%;	Pred. NO. 6.7e-85;								
	Matches 401;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;						
	1 atgcgtgctcaagtatcagccacgaaggcggtgcggccgccgccttgggttcaccatcgaga 60										
	Db 423 ATGTCGTGCGCTCAAGATTATGGCCGCCAGCGGTGCNCNCCGCTTGATGATCAGAGAA 364										
	61 ctggagagacaagagactcgtcggcaaaagcggttcggcacaaagtctcgggagcaaac 120										
	Db 363 CTGAGAACCAAGAAGCTCGTCCGCAAGCGGGTTCCGCCACAGTGTCCGGGCCAACCAT 304										
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Db 243 GTCAGGCCATGGCAACGTCTGGATTAAACAATTCCTGCTCGCCCTAAGACGGGTATTCCAG 184
 Oy 241 AAGTGAACCTGGAGAACCAAGATCCCAGGCAGCCTCTGGTGAACCTTAATTCATGAGAAACGGC 300
 Db 183 AAGTGAACTCGGGACCAAGATATCCCAAGCCGGCTCTGGTTGACTAAATTCAATGAGAAACGGC 124
 Oy 301 TCCCTCTGGGGAGCTGTCTGCAgTcCcaagTgcCcttggcccttgcccgttcctctttgccccctg 360
 Db 123 TCCTGTGCGGGCGCGCTGACGTCCAGTCCAGAGCCCTTGCGCCCTGGCGGCTCTTTCGCGCCTG 64
 Oy 361 CTGAAGAAGTGGTGTCTGGTAGTgTtttaCcttgacagCaaccaagaaccggTgctcc 415
 Db 63 CTCGAAGACAGTGCTGCTTGCGATGTTTTTACCCTGCACACATATACATGAGGGCGTCC 9

RESULT 12
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 DEFINITION mRNA sequence.
 ACCESSION BI905455
 VERSION BI905455.1 GI:16167978
 KEYWORDS EST.
 SOURCE house mouse,
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniala; Vertebrate; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 906)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN).
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 plate: LLM11646 row: n column: 11
 High quality sequence start: 28
 High quality sequence stop: 807.
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 /tissue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Lung; Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5' TGTTTCACATCTCAAGTCGAGCGAGCGCGCCCTGCTGTTTTTTTTTTTTT 3'] Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 188 a 245 c 265 g 208 t

ORIGIN

Query Match 24.9% Score 388.4; DB 10; Length 906;
 Best Local Similarity 74.7%; Fred. No. 2.e-87;
 Matches 560; Conservative 0; Mismatches 171; Indels 19; Gaps 5;

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 451)
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsumura,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc.Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202863
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?I-Rc6t2-RC6-ET0081- 1307080-011-H04kt3-2000-07-13&t4=1) Seq primer: puc 18 forward High quality sequence start: 16 High quality sequence stop: 206. Location/Qualifiers 1. 451 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="ET0081" /date_stage="Adult" /note="Organ: lung-tumor; Vector: puc18; Site:1: Smat; Site_2: Smat; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT	96 a 117 c 139 g 98 t 1 others
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Oy	65 agaacccaggagcccgctcggaagaagaaggcttcggacaagtcttcggcgacacattgga 124
Db	97 AGAACCAAGACCTCCTCGGCMAAGGGGGGTTTGGCCACAGTGTCCGGGCGCACATAGGA 156
Oy	135 agtggagctcagatgtagcggtcgtaaatcgtaactcgaaagcgatatccaagggaagica 184
Db	157 AGTGGGCTACGAGTAGCGTCGCTCAAGATTGTAACCTCCAGAAGCGATATCCAGTAGGCTCA 216
Oy	185 aggcacatgcgaagtcctggataacgaaacctcgctgtctgcctcgtaaagggttatcgagaag 244
Db	217 AGCCGATCGCAAGCTGTGATAAACAATTCGTGCTCCGCCCTGAAGAGGGGTTATGCAAGAG 276
Oy	245 tgaaactggagccaaagatcccaaacggcgctctgtatcaactaaattatgatgaaaacggctccc 304
Db	277 TGAACGTGGACCAAAGATCTTAACCCTGGCTCTGGAAGACTTAATTAATGATGAACGGCTCCT 336
Oy	305 ttctcgagctgctgtagcagctcccaagtgccctcgagccctgacgagctcctcttgcgcgcctgcta 364

Db	337	TGTCGTGGCGCTGCAGACGTCCCAATGCCCTCCTGGCCCTTGCTTGGCGGCTGACTGA	396
Oy	365	aagaagatggtcttggagabgtttacttcgcacgaaccgaaccgagt	411
Db	397	AAGAAGTGTGCTTGGATGTTTACCTGCACAGCATATACCTAAG	443
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DEFINITION	RC6-ET0081-070800-013-BL2 ET0081 Homo sapiens cDNA, mRNA sequence.		
ACCSSION	BF359467		
VERSION	BF359467.1	GI:11318448	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 388) Das Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R., Negel,M.A., de Silveira,W.Jr., Lago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carnevali,A.F., Matsushima,A., Balz,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
JOURNAL	CONTACT: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil		
MEDLINE	20202663		
COMMENT	tel: +55-11-2704922 fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PABESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6et2-RC6-ET0081- 070800-013-BL2c3-2000-08-07et4=1) seq primer: puc 18 forward High quality sequence start: 27 High quality sequence stop: 315. Location/Qualifiers 1..388 /organism="Homo sapiens" /db_xref="Erxon:3606" /clone_lib="ET0081" /dev_stage="Adult" /note="Organ: Lung_tumor; Vector: puc18; site_1: SmaI; site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	79 a 126 c 102 g 81 t		
ORIGIN			
Query Match	23.1%; Score 359.6; DB 10; Length 388;		
Best Local Similarity	96.3%; Pred. No. 2.ee-80;		
Matches 368; Conservative 0; Mismatch 14; Indels 0; Gaps 0;			
Oy	30	tgcgcccgccccccttggtgtccatgataggaaactgagaaacacagagactcgtcgcacaaga	89
Db	388	TGCCCCCGCCCCTTGTTGTTCATCGAGAGACTTGAAACCCAGAGACTGTGGCAAAG	329
Oy	90	cggagttcgcacagtgattccggcgcaacataggaaagtgggtctacagatgtagcggtcaa	149
Db	328	CGGATTCCGACAGTTCCTCCGGCGCAACAATGAGAAAGTGGGGCTTACGATGTGACCTCAA	269

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OY 150 gacgfaaacgagaggaatataccagggaggtcaaggccatgagcaagtctgataaga 209
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OY 210 atcgtgttcgagccctagaaggggtatcgaagaagtgaaactggaaccaagatcccaagcc 269
Db 208 ATTCGTGCTGCGCCTAGAAAGGGGTTATCGAAGAGTGAACTGGGACCAGATCCCAAGCC 149
OY 270 ggcctcgtgactaaatcatgagaaagcgtccctgtcggggctgtgcaatgccaatg 329
Db 148 GCGTCTGCTGACTAAATTCATGAGAAAGCGCTCCTTGTCAAGCGCTGCTCAGTCCAGTG 89
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OY 390 cctgcagacagaaaccggtg 411
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Search completed: August 13, 2002, 20:36:21
Job time: 2169 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 20:04:37 ; Search time 2051.96 Seconds
(Without Alignment)
15878.778 Million cell updates/sec

Title: US-09-762-491-5

Perfect score: 1557
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb-hlg: *
3: gb-in: *
4: gb-om: *
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8: gb-pl: *
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22: em-ov: *
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25: em-pl: *
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29: em-vi: *
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31: em-hlg-inv: *
32: em-hlg-other: *
33: em-higo-inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description

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2	1548.6	99.5	1557	6	AR105328	AR105328 Sequence
3	1548.6	99.5	1557	6	AX067677	AX067677 Sequence
4	1536.4	98.0	1873	6	AR105327	AR105327 Sequence
5	1526.4	98.0	1873	6	AX067676	AX067676 Sequence
6	673.6	43.3	1437	6	AX100029	AX100029 Sequence
7	672.2	42.0	2015	10	AF036537	AF036537 Rattus no
8	654.2	42.0	1833	10	AF178953	AF178953 Mus muscu
9	377.6	24.3	196533	9	CNS007V1	CNS007V1 human chr
10	379.6	21.2	1073	6	AX056439	AX056439 Sequence
11	193.6	12.4	240105	6	AC098877	AC098877 Mus muscu
12	135.8	8.7	254	6	AX211236	AX211236 Sequence
13	109	7.0	3876	9	AR027424	AR027424 Homo sapi
14	107.4	6.9	3879	9	HSAT78016	HSAT78016 Homo sapi
15	107.4	6.9	3882	9	AB047783	AB047783 Homo sapi
16	104	6.7	2499	6	AX166548	AX166548 Sequence
17	95.2	6.1	3559	10	AF302127	AF302127 Mus muscu
18	88.4	5.7	2348	6	AX207411	AX207411 Sequence
19	74	4.8	124516	9	AP001615	AP001615 Homo sapi
20	74	4.8	219256	9	AP001743	AP001743 Homo sapi
21	73.2	4.7	139651	2	OSJN00183	OSJN00183 Oryza sat
22	71.8	4.6	144720	8	AC087544	AC087544 Oryza sat
23	71.8	4.6	193068	8	AP003455	AP003455 Oryza sat
24	68.4	4.4	3897	1	NCU40656	NCU40656 Oryza sat
25	63.4	4.1	2837	3	ACU67056	ACU67056 Acanthamoeb
26	63.2	4.1	177034	9	AP002840	AP002840 Homo sapi
27	63.2	4.0	152859	2	AC096518	AC096518 Rattus no
28	62.8	4.0	120538	2	AP004082	AP004082 Oryza sat
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ALIGNMENTS

RESULT 1
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LOCUS AF156884
DEFINITION Homo sapiens RIP-like kinase (RIP3) mRNA, complete cds.
ACCESSION AF156884
VERSION AF156884.1 GI:5059424
KEYWORDS

SOURCE

human.
Homo sapiens

REFERENCE

1 (bases 1 to 1557)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS

Yu, P.W., Huang, B.C., Shen, M., Quast, J., Chan, E., Xu, X., Nolan, G.P.,
Payan, D.G. and Luo, Y.

TITLE

Identification of RIP3, a RIP-like kinase that activates apoptosis
and NF-kappaB

JOURNAL

Curr. Biol. 9 (10), 539-542 (1999)

MEDLINE

99272740

AUTHORS

Yu, P.W., Huang, B.C., Shen, M., Quast, J., Chan, E., Xu, X., Nolan, G.P.,
Payan, D.G. and Luo, Y.

TITLE

Direct Submission
Submitted (04-JUN-1999) Rigel, Inc. 240E Grand Ave., San Francisco,

CA 94080, USA
FEATURES
Location/Qualifiers
source 1..1557
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BASE COUNT 397 a 424 c 446 g 290 t
ORIGIN

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QY 61 ctggagaaacgaagacgtctgcgcaaaacggttcgcaagtggtccggcgcaaat 120
DB 61 CTGGAGAACCAAGACCTGTGCGCAAAAGCGGTTCGCGACAGTGTCCGGCGCAACAT 120
QY 121 aggaagctggggtcagatgtgtgcgaagaatcgtaaacctcgaagcgaatccagagag 180
DB 121 AGGAAGTGGCGCTACGATGTGCGGTCAAGTCTAAGTCAAGCGCATATCCAGGAG 180
QY 181 gtcaagcgcatgcaagtcctgtgataaagaatcgtgttcgctagaagggctatcag 240
DB 181 GTCAAGCGCATGCAAGTCTGTGATTAAGCAATTCGTGTGCGCTTAAGGGGTATACAG 240
QY 241 aaggtgaacctgggaacaaagatcccaagccggctctgtgtgataatcattcgaagagcg 300
DB 241 AAGGTGAACCTGGACCAAGATCCCAAGCCGGCTGTGTGATTAATTCATGGAGAACGCG 300
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DB 301 TCCCTGTGCGGGCTGTGCAATCCCAAGTCCCTGCGCTGCGCTCTTGTCCGCGCTG 360
QY 361 ctgaagaagatggtgtgtctgtggaatgttcaacctgcagcaacgaagaccgggtgctctgac 420
DB 361 CTGAAGAAGATGCTGTGCTGTGATTTTACCTGCACACCAAGAACCGGTGTCTCTGAC 420
QY 421 cgggaccccaagcattcgaacgtctcgggaacccagagatgtgaagctcaagctgacagat 480
DB 421 CGGGAACCTCAAGCCATCCAAAGTCTCTGCGGACCCAGAACCTGCACACTCAAGCTGCAAGT 480
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DB 601 GCCAAGTGAAGCTTCAAGCTTCGGGATACCTTAATGCGGCACTGCTTCTCGAAGAGAAATT 660

DB 601 GCCAAGTGAAGCTTCAAGCTTCGGGATCTTAATGCGGCACTGCTTCTCGAAGAGAAATT 660
QY 661 gagttccaaacgaacacatcactcgtgtgaagcagtgatgaagcaggaacggcgct 720
DB 661 GAGTTCCCAACCAACCAATCACTCTGTACCAACCACTGTCACACGAGCAAGCGGCT 720
QY 721 tcaatgctgaagctgcccgaagcggcgtgagaccccggtctgaagaagatgaagag 780
DB 721 TCATGTGCTGAGTGGCCCAAGCCGGGCTGAGACTCCGGCTTAAAGATGAAGAGAG 780
QY 781 ctaattgaagctcgtcggagcagtgtagcccaagagacagaccctctccagaagatgctc 840
DB 781 CTAATGACGCTCTGCTGGAGCAGTAGCCCAAGGACAGACCTCTCTTCCAGAAATGCTA 840
QY 841 ccaaaacatgaagatcttcagatggttgagaaacaataatgaatgctgtgtctcagc 900
DB 841 CCAAAACATGATCAATCTTCAGATGTTGAGAAACATATGTAATCTCTCTCTCCACG 900
QY 901 gtaagaatctcgtcgtcagctcagaagcagcaataatgaatgctgtgtctcagag 960
DB 901 GTAAGAATTTCTGCTCTCAGCTCAAGACGAAATGAGATTTTCTATCCCAAGTCA 960
QY 961 ggcgaagagagcagaatgagatgtgtttagggaaaccaatgaataacagacatcgt 1020
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RESULT 2
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LOCUS AR105328 1557 bp DNA Linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6096539.
ACCESSION AR105328
VERSION AR105328.1 GI:12818925
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1557)
 AUTHORS Gomes, B. Charles., Kasof, G. M. and Prosser, J. Caroline.
 TITLE Protein activator of apoptosis
 JOURNAL Patent: US 6096539-A 2 01-AUG-2000;
 FEATURES Location/Qualifiers

SOURCE

1.1557

BASE COUNT 395 a 422 c 448 g 291 t 1 others
 ORIGIN

Query Match 99.5% Score 1548.6; DB 6; Length 1557;
 Best Local Similarity 99.6% Pred. No. 0;
 Matches 1551; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 1 atgtcgtgcttcaagttatgtccagcgtgtcccccgttctgtgtctcctcagaa 60
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 Db 841 CCAAAAACCTGAGAGCTCTCAGAGATGTGAGAAACATATGAATGCTGCTCCTCACG 900

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RESULT 3
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 LOCUS AK067677 1557 bp DNA linear PAT 19-JAN-2001
 DEFINITION Sequence 2 from Patent WO0077200.
 ACCESSION AK067677
 VERSION AK067677.1 GI:12329571
 KEYWORDS

SOURCE

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1557)

AUTHORS Gomes, B. C., Kasof, G. M. and Prosser, J. C.

TITLE Receptor interacting protein rip3

JOURNAL Patent: WO 0077200-A 2 21-DEC-2000;

Astrazeneca AB (SE)

Location/Qualifiers

SOURCE

1.1557

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 395 a 422 c 448 g 291 t 1 others

ORIGIN

Query Match 99.5% Score 1548.6; DB 6; Length 1557;
 Best Local Similarity 99.6% Pred. No. 0;

Matches 1551; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 1 ATGTCTGGCTCAATGTTATGGCCAGCGGTGCCCCCCTTGGTGTCAATGAGAA 60
Oy 61 ctggaaacacagagctcgttcgcaaaagcgttcgcaagtgctcggcgcaaat 120
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Oy 541 ggcacccctggagctcgttcgcaaaactgtgttcaagcaaaacgagagcctccaca 600
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Oy 1441 ccttcgggcaagagagagagagagagagagagagagagagagagagagagagagagag 1500
Db 1441 CCTTCGGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Oy 1501 aagaatccttaagagagagagagagagagagagagagagagagagagagagagagag 1557
Db 1501 AAGATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557

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RESULT 4
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LOCUS AR105327
DEFINITION Sequence 1 from patent US 6096539.
ACCESSION AR105327
VERSION AR105327.1 GI:12818924
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1873)
AUTHORS Gomes,B,Charles., Kasof,G.M. and Prosser,J.Caroline.
TITLE Protein activator of apoptosis
JOURNAL Patent: US 6096539-A 1 01-AUG-2000.
FEATURES
Source 1..1873
BASE COUNT 471 a 531 c 518 g 353 t
ORIGIN

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Query Match 98.04; Score 1526.4; DB 6; Length 1873;
Best Local Similarity 99.19; Pred. No. 0;
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Oy 121 aggaagtcgggtcagatgtgctgagtcgaagtcgtaaacctcgaagcgatataccagagag 180
Db 121 AGGAAGTGGGGTACGATGTGGCGGTCAAGTCTTAACCTGGAAGCGAATACAGAG 344
Oy 181 gtcgaagcagtcgcaagctcgtgataagaaatcgtgtcgcgcctagaaggggtatcag 240

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Dh	405	AAAGTCGCGCGGTCCAGGCGCAAGATCCCAAGCGCGCTCTGGTGAATTAATTCATGAGGAAC	464
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Qy	418	caacgggagctcaagccatccaaagctctcgcggaccacgaagctctgacgctcgaagcttgaca	477
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DEFINITION	Sequence 1 from Patent WO0077200.				
ACCESSION	AX067676				
VERSION	AX067676.1	GI:12339570			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Plimates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1873)				
AUTHORS	Gomes,B.C., Kasof,G.M. and Prosser,J.C.				
TITLE	Receptor Interacting Protein ri3				
JOURNAL	Patent: WO 0077200-A 1 21-DEC-2000; AstraZeneca AB (SE)				
FEATURES	location/Qualifiers				
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BASE COUNT	471 a 531 c 518 g 353 t				
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RESULT 6
AX100029 AX100029 1437 bp DNA linear PAT 02-APR-2001
LOCUS Sequence 1 from Patent WO0119990.
DEFINITION AX100029
ACCESSION AX100029
VERSION AX100029.1 GI:13539035
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1437)
AUTHORS Virca G.D. and Bird T.A.
TITLE Rip3-Like death-associated kinase
JOURNAL Patient: WO 0119990-A 1 22-MAR-2001;
IMMUNEX CORPORATION (US)
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DB	AUTHORS	Chen,K.H. and Tang,J.
TITLE		A hemocysteine-responder gene cloned from WKI VSMCs by differential display
JOURNAL		Unpublished
REFERENCE		2 (bases 1 to 2015)
AUTHORS		Chen,K.H. and Tang,J.
JOURNAL		Submitted (03-DEC-1997) Institute of Cardiovascular Research, Beijing Medical University, Xueyuan Rd. 38, Beijing 100083, China
REFERENCE		3 (bases 1 to 2015)
AUTHORS		Chen,K.H. and Tang,J.
JOURNAL		Direct Submission
TITLE		Submitted (21-MAY-2001) Institute of Cardiovascular Research, Beijing Medical University, Xueyuan Rd. 38, Beijing 100083, China
REMARK		Sequence update by submitter
COMMENT		On May 21, 2001 this sequence version replaced gi:4104520.
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RESULT 8
LOCUS AF178953
DEFINITION Mus musculus receptor interacting protein 3 (Rip3) mRNA, complete
ACCESSION AF178953
VERSION AF178953.1
KEYWORDS GI:6063100
SOURCE
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  Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
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  1 (bases 1 to 1833)
  Padermik, N.J., Donner, D.B., Goebel, M.G. and Harrington, M.A.
  Mouse Interacting Protein 3 Does Not Contain a Caspase-Recruiting
  Or a Death Domain but Induces Apoptosis and Activates NF-kappaB
  Mol. Cell. Biol. 19 (1999) In press
  2 (bases 1 to 1833)
  Padermik, N.J., Donner, D.B., Goebel, M.G. and Harrington, M.A.
  Direct Submission
  Submitted (19-AUG-1999) Walther Oncology Center, Indiana University
  School of Medicine, 1044 West Walnut Street, Indianapolis, IN
  46202, USA

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D	1249	GACACATCATGTTGGGCTGGCCACACACAGCAAGAGACATCTTGAGACCCCGTGGTGGACT	1308
O	1186	cccccaaacccagagacctcaacttcaagaaaccaaagatgagccagccctactcaactatga	1245
D	1309	CTCTACATCTCCAAATCTTACCTTTGAGAGGCACAAACCTGGGCAAGCTTTACTTGAC	1366
O	1246	acacaaagctctgnaaccccgaggaatcaagggggctgtgagagcaagagcatgaactgtctc	1305

Db 1369 ACCTCCGCTCTCACCCCCAAAAGAAATCAGGAGAAATGAAAGACAGCCGACTCTGGTAT 1428

Qy 1306 tgcaggaagcccccgcagagcaaatccagtaacagagcgacgcgcctcgtaatacataaactgac 1365

Db 1429 CCTGTGAGACCC--ACGAAATTCMAATGACAGGGCCACCGGCTCTCTCTTCMAACATGT 1485

Qy 1366 tctgagggctgcagagcttgagagcaacaactactgactatgcaatgcagacgaactgc----- 1418

Db 1486 TCTGGAAGTGCAGATTTGGGAACCTGCACAACTCTTGGGTACACACACAGAAACTGACGGCTCA 1545

Qy 1419 --ctgtccacatacggggctctgcagactctgcggaccttcggagagggagggctctgcagaccacca 1476

Db 1546 AGTTTGGCCAAAGTATGACCCAMGACACAGTTTGGCGAGGGGTAGGGGGCTGGCGAGC-CCTTCCA 1604

Qy 1477 ccagtaggtctgcagaagaagccctaaagaatcctgaacccg 1517

Db 1605 CAGGTGACCTTCAAGAAATGCATCTGCACAGACCTGAATGTG 1645

RESULT	9	
CNS000YI	CNS000YI	196533 bp DNA linear PRI 04-JUL-2001
LOCUS		Human chromosome 14 DNA sequence BAC R-93489 of library RGC1-11
DEFINITION		from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION	AL096870	
VERSION	AL096870.5	GI:14625739
KEYWORDS	HTG; HTGS; ACTIVEFIN.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
1 (bases 1 to 196533) Helliger, R., Pettit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Attguenave, F., Levy, M., Eschenberg, R., Bruls, T., debernardinis, V., Crund, C., Gyapay, G., Saurin, W. and Weissenbach, J.	Genoscope - Centre National de Sequencage Submitted (04-JUL-2001)
2 (bases 1 to 196533) Genoscope.	Submitted (04-JUL-2001)

COMMENT

Center: Genoscope / Centre National de Séquençage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: segret@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-80A15 (AC-AL132800)
Downstream BAC (overlapping the SP6 end) : R-468E2 -----
Summary Statistics
Assembly program: Phrap, version 2.0
Quality coverage: 9.97x in Q20 bases; sum-of-contigs

Overall quality chart :	
Range	bases
0	:
1 - 9	:
10 - 19	:
20 - 29	:
30 - 39	:
40 - 49	:
50 - 59	:
60 - 69	:
70 - 79	:
80 - 89	:
90 - 99	:
	16
	48
	1585
	6383
	10286
	25557
	61534
	91204

FEATURES source	Percentage of bases with a quality value >= 40 : 99 %.	Location/Qualifiers
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STS	53793.53918	/note="matching EMBL:AA27560 Rdb:RH91896 dbSTS:STS64900 Identified using the e-PCR software (G. Schuler)"
STS	71412.71564	/note="matching EMBL:AA044828 Rdb:RH93999 dbSTS:STS66992 Identified using the e-PCR software (G. Schuler)"
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STS	81788.82011	/note="matching EMBL:AA009760 Rdb:RH75263 dbSTS:STS52351 Identified using the e-PCR software (G. Schuler)"
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STS	95021.99159	/note="matching EMBL:H22572 Rdb:RH78575 dbSTS:STS55316 Identified using the e-PCR software (G. Schuler)"
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LOCUS		AK027424	3876 bp mRNA linear PRI 15-MAY-2001
DEFINITION		Homo sapiens CDNA FLJ14518 fls, clone NT2M100850, weakly similar to ANKRYRN R.	
ACCESSION		AK027424	
VERSION		AK027424.1	GI:16042089
KEYWORDS		oligo capping; fls (full insert sequence).	
SOURCE		Homo sapiens testis/carcinoma cell line:NT2 CDNA to mRNA, clone_11b:NT2RM1 clone:NT2M100850.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
AUTHORS		1 (aites)	
JOURNAL		Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Matsushima,M., Hosokiri,T., Kaki,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Taguchi,S., Matanabe,S., Kimura,K., Murakami,K., Iishi,S., Kawai,T., Salto,K., Yamamoto,J., Makatsuta,A., Nakamura,Y., Nagamori,K., Maehio,Y., Ninomiya,K. and Iwayanagi,T.	
TITLE		NDO human cDNA sequencing project	
AUTHORS		Unpublished	
TITLE		2 (bases 1 to 3876)	
JOURNAL		Isogai,T. and Otsuki,T.	
AUTHORS		Direct Submission	
TITLE		Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genom@helix.co.jp, Tel:81-438-52-3931, Fax:81-438-52-3952)	
JOURNAL		NDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'-3' end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.	
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ORIGIN			

[illegible]

TITLE Gschwendt, M.
DIR. A NOVEL PROTEIN KINASE THAT INTERACTS WITH PROTEIN KINASE
CDELTAS. CLONING, CHARACTERIZATION, AND GENE ANALYSIS
JOURNAL J. Biol. Chem. 275 (46), 36350-36357 (2000)
PUBLISHED 10948194
REFERENCE 2 (bases 1 to 3879)
AUTHORS Gschwendt, M.
TITLE Direct Substitution
Submitted (18-MAY-2000) Gschwendt M., Biochemistry of
Tissue-Specific Regulation, German Cancer Research Center, Im
Neuenheimer Feld 280, D-69151 Heidelberg, GERMANY

FEATURES

Source Location/Qualifiers
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RESULT 15
AB047783 3882 bp mRNA linear PRI 30-MAY-2001
LOCUS AB047783
DEFINITION Homo sapiens ANKRD3 mRNA for dual-specificity Ser/Thr/Tyr kinase.
ACCESSION AB047783
VERSION AB047783.1 GI:14245728
KEYWORDS
SOURCE Homo sapiens fetal kidney and fetal lung cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases)
AUTHORS Shimizu, N., Kudoh, J. and Shibuya, K.
TITLE Homo sapiens mRNA for ANKRD3, complete cds
JOURNAL Published Only in Database (2001) in press
REFERENCE 2 (bases 1 to 3882)
AUTHORS Shimizu, N., Kudoh, J. and Shibuya, K.
TITLE Direct Substitution
Submitted (25-AUG-2000) Nobuyoshi Shimizu, Keio University, School
of Medicine, Japan B-mail: shimizun@med.keio.ac.jp,
Tel: 81-3-3351-2310, Fax: 81-3-3351-2310)

FEATURES

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 21:14:38 ; Search time 24.14 Seconds
(without alignments) 525.140 Million cell updates/sec

Title: US-09-762-491-6

Sequence: 1 MSCVKLMPGAPAPLVISIE.....PKOPEAMSRQGWYNSGKZ 519

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum Db seq length: 0
Maximum Db seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/ptodaca/1aa/5A.COMB.pep.*
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6: /cgn2_6/ptodaca/1aa/5F.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2750	99.1	518	3	US-09-329-418-3
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3	2747	99.0	518	3	US-09-329-418-5
4	2747	99.0	518	4	US-09-531-914-5
5	2742	98.8	518	4	US-09-329-418-4
6	2742	98.8	518	4	US-09-531-914-4
7	2732	98.1	518	3	US-09-329-418-9
8	2722	98.1	518	4	US-09-531-914-9
9	2145.5	77.3	420	3	US-09-329-418-8
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11	1358	49.0	261	3	US-09-329-418-6
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13	1305	47.0	240	3	US-09-329-418-7
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16	445.5	16.1	656	4	US-09-069-023-28
17	423	15.2	671	1	US-09-132-118-2
18	423	15.2	671	4	US-08-444-005-17
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20	379	13.7	531	4	US-09-069-023-1
21	379	13.7	540	3	US-09-019-942-1
22	379	13.7	540	4	US-09-099-023-27
23	379	13.7	540	4	US-09-069-023-27
24	376	13.6	336	4	US-09-188-930-185
25	376	13.6	300	4	US-09-099-041A-4
26	376	13.6	330	4	US-09-069-023-3
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31	302	10.9	263	4	US-09-390-425-5	Sequence 5, Appl1
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33	302	10.9	821	1	US-08-003-3118-2	Sequence 2, Appl1
34	302	10.9	821	1	US-08-261-432-2	Sequence 2, Appl1
35	302	10.9	821	5	US-08-357-533A-10	Sequence 10, Appl1
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45	287.5	10.4	516	3	US-08-459-951-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-329-418-3
Sequence 3, Application US-09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70516
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Fastseq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 518
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-329-418-3

Query Match	99.1%	Score	2750	DB 3	Length	518			
Best Local Similarity	99.4%	Pred. No.	1.7e-210						
Matches	515	Conservative	1	Mismatches	2	Indels	0	Gaps	0
Qy	1	MSCVKLMPGAPADLVISIEELENOELVKGDFCTVRPAORHRCVAVAKYNSKASRE	60						
Db	1	MSCVKLMPGAPADLVISIEELENOELVKGDFCTVRPAORHRCVAVAKYNSKASRE	60						
Qy	61	VKMAASLDNEFTVLRLEGYTERVMDQPKALVTKRMENGSUSGLQSCPPFPLCRL	120						
Db	61	VKMAASLDNEFTVLRLEGYTERVMDQPKALVTKRMENGSUSGLQSCPPFPLCRL	120						
Qy	121	LKEVYGNFTYLDQNPVLLHRDLKPSNVLPDPLAVKLAIDFGISTFGGSGSGSGGPG	180						
Db	121	LKEVYGNFTYLDQNPVLLHRDLKPSNVLPDPLAVKLAIDFGISTFGGSGSGSGGPG	180						
Qy	181	GTGTYAPLPEFVNVNRKSTASDVYSFGIILMAVLAGEVELPTBPSLYAVACRORNP	240						
Db	181	GTGTYAPLPEFVNVNRKSTASDVYSFGIILMAVLAGEVELPTBPSLYAVACRORNP	240						
Qy	241	SLAELPQAPPEPGLEGLKELMQLCNSSEKDRPSFDECLPTDDEVFQVNNNAVST	300						
Db	241	SLAELPQAPPEPGLEGLKELMQLCNSSEKDRPSFDECLPTDDEVFQVNNNAVST	300						
Qy	301	VNDFTLSQSSNRNRSIPESGGCTEDGFRRTIENQSRNDVNVSEMLNTLKEEPSS	360						
Db	301	VNDFTLSQSSNRNRSIPESGGCTEDGFRRTIENQSRNDVNVSEMLNTLKEEPSS	360						
Qy	361	VPKKCSLTKRRAQEEVQVAVAGTSSDMAQPPQETSTFNNQMPSTSTCTGTPSG	420						
Db	361	VPKKCSLTKRRAQEEVQVAVAGTSSDMAQPPQETSTFNNQMPSTSTCTGTPSG	420						

07 421 PRNGAGAEKGMNSCRTPPEPNPTGRLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
|||||
Db 421 PRNGAGAEKGMNSCRTPPEPNPTGRLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
07 481 PSCKGRGLQHPPEVSGSGCPDPEANRPGQWYHNSCK 518
|||||
Db 481 PSCKGRGLQHPPEVSGSGCPDPEANRPGQWYHNSCK 518

RESULT 2

US-09-531-914-3
: Sequence 3, Application US/09531914
: Patent No. 6267956
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/531.914
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 09/329,418
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FASTSEQ for Windows version 3.0
: SEQ ID NO 3
: LENGTH: 518
: TYPE: PRT
: ORGANISM: Homo Sapiens
US-09-531-914-3

Query Match 99.1%, Score 2750; DB 4; Length 518;
Best Local Similarity 99.4%; Pred. No. 1,7e-210;
Matches 515; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

07 1 MSCVTLMPGAPAPLVSTIEELNDELGVKDGFGTVFRAQHRKMGDYAVKIVNSKAISRE 60
|||
Db 1 MSCVTLMPGAPAPLVSTIEELNDELGVKDGFGTVFRAQHRKMGDYAVKIVNSKAISRE 60
07 61 VKAASLDNEFVLRLEGVIEFVNNDOPKRALVTKFMENSGISGLQSCPRPPLLCRL 120
|||||
Db 61 VKAASLDNEFVLRLEGVIEFVNNDOPKRALVTKFMENSGISGLQSCPRPPLLCRL 120
07 121 LKEVYLGMEFLHDONPVLLHDLKPSNVLPDPELVKLADELSTFGSGSGSGSGEPG 180
|||||
Db 121 LKEVYLGMEFLHDONPVLLHDLKPSNVLPDPELVKLADELSTFGSGSGSGSGEPG 180
07 181 GTLGLAPLPELVNVRKASTASDVYSGILMAVLAGREVELPTEPSLVYEAVCNRQNRP 240
|||||
Db 181 GTLGLAPLPELVNVRKASTASDVYSGILMAVLAGREVELPTEPSLVYEAVCNRQNRP 240
07 241 SLAELPQAGPETPGLEGLKELMQLCHNSSEPRDPSFOBELPKTDEVFOYENNNAAVST 300
|||||
Db 241 SLAELPQAGPETPGLEGLKELMQLCHNSSEPRDPSFOBELPKTDEVFOYENNNAAVST 300
07 301 VMDPFLSOLKSSNRFPSTIPESGOGGTENDGFRRTIENHSHNDVNSDKLNLEEPS 360
|||||
Db 301 VMDPFLSOLKSSNRFPSTIPESGOGGTENDGFRRTIENHSHNDVNSDKLNLEEPS 360
07 361 VPKKPSLTKRSLKRAQEEVPOAMTAGTSSDSMAOPQTPETSTFRNQPSTSTGTPSPG 420
|||||
Db 361 VPKKPSLTKRSLKRAQEEVPOAMTAGTSSDSMAOPQTPETSTFRNQPSTSTGTPSPG 420
07 421 PRNGAGAEKGMNSCRTPPEPNPTGRLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
|||||
Db 421 PRNGAGAEKGMNSCRTPPEPNPTGRLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
07 481 PSCKGRGLQHPPEVSGSGCPDPEANRPGQWYHNSCK 518
|||||
Db 481 PSCKGRGLQHPPEVSGSGCPDPEANRPGQWYHNSCK 518

RESULT 3

US-09-329-418-5
: Sequence 5, Application US/09329418
: Patent No. 6096539
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/329,418
: PRIOR FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FASTSEQ for Windows version 3.0
: SEQ ID NO 5
: LENGTH: 518
: TYPE: PRT
: ORGANISM: Dactylolaccal Sequence
: FEATURE:
: OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-5

Query Match 99.0%, Score 2747; DB 3; Length 518;
Best Local Similarity 99.2%; Pred. No. 2,9e-210;
Matches 514; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

07 1 MSCVTLMPGAPAPLVSTIEELNDELGVKDGFGTVFRAQHRKMGDYAVKIVNSKAISRE 60
|||
Db 1 MSCVTLMPGAPAPLVSTIEELNDELGVKDGFGTVFRAQHRKMGDYAVKIVNSKAISRE 60
07 61 VKAASLDNEFVLRLEGVIEFVNNDOPKRALVTKFMENSGISGLQSCPRPPLLCRL 120
|||||
Db 61 VKAASLDNEFVLRLEGVIEFVNNDOPKRALVTKFMENSGISGLQSCPRPPLLCRL 120
07 121 LKEVYLGMEFLHDONPVLLHDLKPSNVLPDPELVKLADELSTFGSGSGSGSGEPG 180
|||||
Db 121 LKEVYLGMEFLHDONPVLLHDLKPSNVLPDPELVKLADELSTFGSGSGSGSGEPG 180
07 181 GTLGLAPLPELVNVRKASTASDVYSGILMAVLAGREVELPTEPSLVYEAVCNRQNRP 240
|||||
Db 181 GTLGLAPLPELVNVRKASTASDVYSGILMAVLAGREVELPTEPSLVYEAVCNRQNRP 240
07 241 SLAELPQAGPETPGLEGLKELMQLCHNSSEPRDPSFOBELPKTDEVFOYENNNAAVST 300
|||||
Db 241 SLAELPQAGPETPGLEGLKELMQLCHNSSEPRDPSFOBELPKTDEVFOYENNNAAVST 300
07 301 VMDPFLSOLKSSNRFPSTIPESGOGGTENDGFRRTIENHSHNDVNSDKLNLEEPS 360
|||||
Db 301 VMDPFLSOLKSSNRFPSTIPESGOGGTENDGFRRTIENHSHNDVNSDKLNLEEPS 360
07 361 VPKKPSLTKRSLKRAQEEVPOAMTAGTSSDSMAOPQTPETSTFRNQPSTSTGTPSPG 420
|||||
Db 361 VPKKPSLTKRSLKRAQEEVPOAMTAGTSSDSMAOPQTPETSTFRNQPSTSTGTPSPG 420
07 421 PRNGAGAEKGMNSCRTPPEPNPTGRLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
|||||
Db 421 PRNGAGAEKGMNSCRTPPEPNPTGRLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
07 481 PSCKGRGLQHPPEVSGSGCPDPEANRPGQWYHNSCK 518
|||||
Db 481 PSCKGRGLQHPPEVSGSGCPDPEANRPGQWYHNSCK 518

RESULT 4

US-09-531-914-5
: Sequence 5, Application US/09531914
: Patent No. 6267956
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/531.914
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 09/329,418
: PRIOR FILING DATE: 1999-06-11

NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 518
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-5

Query Match 99.0%; Score 2747; DB 4; Length 518;
Best Local Similarity 99.2%; Pred. No. 2,9e-210;
Matches 514; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 MSCVRLPSCAPAPLVISIELENOELVKGDFGTVFRAQHRKMGIDVAIVSKAISRE 60
1 MSCVRLPSCAPAPLVISIELENOELVKGDFGTVFRAQHRKMGIDVAIVSKAISRE 60
61 VKAASLDNEFVRLBECVIERKVMDDPKPALVTKFMENGSLGILSQCPRPMLLCRL 120
61 VKAASLDNEFVRLBECVIERKVMDDPKPALVTKFMENGSLGILSQCPRPMLLCRL 120
121 LKEVYLGAFYLDQNPVTLHRDLKPSNVLPDELVKYLADGLSTFGGSGSGSGEPG 180
121 LKEVYLGAFYLDQNPVTLHRDLKPSNVLPDELVKYLADGLSTFGGSGSGSGEPG 180
181 GTLGYLAPLELVNVRKASTASDVSTFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
181 GTLGYLAPLELVNVRKASTASDVSTFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
241 SLATLPQACPETPCLBCKELMQLCNSSEPKDRPSFOCLPKTDEVOMENNNAAVST 300
241 SLATLPQACPETPCLBCKELMQLCNSSEPKDRPSFOCLPKTDEVOMENNNAAVST 300
301 VKDLSQLKSSNRRTSIPESGCGTDMQDFRRTIENQHSRDVAVSEKLNKLEEPS 360
301 VKDLSQLKSSNRRTSIPESGCGTDMQDFRRTIENQHSRDVAVSEKLNKLEEPS 360
361 VPKCPSLTKRSRAOEVOVPOANTACTSSDMAOPOTPETSTRNOMPSTSTGTPSPG 420
361 VPKCPSLTKRSRAOEVOVPOANTACTSSDMAOPOTPETSTRNOMPSTSTGTPSPG 420
421 PRGNGAEROGAMNSCRTPENPVYGRPLVNTYNCSGVQVDNNYLTMOQTALPTMGLA 480
421 PRGNGAEROGAMNSCRTPENPVYGRPLVNTYNCSGVQVDNNYLTMOQTALPTMGLA 480
481 PSKGRGLQHPPPVSGSGEPKDEPANSRPOGTYNHSK 518
481 PSKGRGLQHPPPVSGSGEPKDEPANSRPOGTYNHSK 518

RESULT 5
US-09-329-418-4
Sequence 4, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329.418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 518
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-4

Query Match 98.8%; Score 2742; DB 3; Length 518;
Best Local Similarity 99.2%; Pred. No. 7.3e-210;
Matches 514; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 MSCVRLPSCAPAPLVISIELENOELVKGDFGTVFRAQHRKMGIDVAIVSKAISRE 60
1 MSCVRLPSCAPAPLVISIELENOELVKGDFGTVFRAQHRKMGIDVAIVSKAISRE 60
61 VKAASLDNEFVRLBECVIERKVMDDPKPALVTKFMENGSLGILSQCPRPMLLCRL 120
61 VKAASLDNEFVRLBECVIERKVMDDPKPALVTKFMENGSLGILSQCPRPMLLCRL 120
121 LKEVYLGAFYLDQNPVTLHRDLKPSNVLPDELVKYLADGLSTFGGSGSGSGEPG 180
121 LKEVYLGAFYLDQNPVTLHRDLKPSNVLPDELVKYLADGLSTFGGSGSGSGEPG 180
181 GTLGYLAPLELVNVRKASTASDVSTFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
181 GTLGYLAPLELVNVRKASTASDVSTFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
241 SLATLPQACPETPCLBCKELMQLCNSSEPKDRPSFOCLPKTDEVOMENNNAAVST 300
241 SLATLPQACPETPCLBCKELMQLCNSSEPKDRPSFOCLPKTDEVOMENNNAAVST 300
301 VKDLSQLKSSNRRTSIPESGCGTDMQDFRRTIENQHSRDVAVSEKLNKLEEPS 360
301 VKDLSQLKSSNRRTSIPESGCGTDMQDFRRTIENQHSRDVAVSEKLNKLEEPS 360
361 VPKCPSLTKRSRAOEVOVPOANTACTSSDMAOPOTPETSTRNOMPSTSTGTPSPG 420
361 VPKCPSLTKRSRAOEVOVPOANTACTSSDMAOPOTPETSTRNOMPSTSTGTPSPG 420
421 PRGNGAEROGAMNSCRTPENPVYGRPLVNTYNCSGVQVDNNYLTMOQTALPTMGLA 480
421 PRGNGAEROGAMNSCRTPENPVYGRPLVNTYNCSGVQVDNNYLTMOQTALPTMGLA 480
481 PSKGRGLQHPPPVSGSGEPKDEPANSRPOGTYNHSK 518
481 PSKGRGLQHPPPVSGSGEPKDEPANSRPOGTYNHSK 518

RESULT 6
US-09-531-914-4
Sequence 4, Application US/09531914
Patent No. 6267956
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/531.914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329.418
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 518
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-4

Query Match 98.8%; Score 2742; DB 4; Length 518;
Best Local Similarity 99.2%; Pred. No. 7.3e-210;
Matches 514; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 MSCVRLPSCAPAPLVISIELENOELVKGDFGTVFRAQHRKMGIDVAIVSKAISRE 60
1 MSCVRLPSCAPAPLVISIELENOELVKGDFGTVFRAQHRKMGIDVAIVSKAISRE 60
61 VKAASLDNEFVRLBECVIERKVMDDPKPALVTKFMENGSLGILSQCPRPMLLCRL 120

DB 61 VKAASLSENEFVLRLEGVIERKVMNDOPKPAVLTAKFKMENGSLGILQSGCPRRPPLICRL 120
QY 121 LKEVYLGMEFYLRHDOHPVTLHRDLKPSNVLPDELYHVKLADGSLTPGCGSGSGSGSGG 180
DB 122 LKEVYLGMEFYLRHDOHPVTLHRDLKPSNVLPDELYHVKLADGSLTPGCGSGSGSGSGG 180
QY 181 GTLGTLAPLPELVNVRKASTASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
DB 181 GTLGTLAPLPELVNVRKASTASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
QY 241 SLAEIPQAGPETPGLGELKELMQLCWSSEPRKPSFOECLPKTDEVFOVEMNNNAVST 300
DB 241 SLAEIPQAGPETPGLGELKELMQLCWSSEPRKPSFOECLPKTDEVFOVEMNNNAVST 300
QY 301 VDFLSQLKSSNRRESIPESGCGGTENDGFRRTIENQHSRDVYVSEMLKLNLEPPSS 360
DB 301 VDFLSQLKSSNRRESIPESGCGGTENDGFRRTIENQHSRDVYVSEMLKLNLEPPSS 360
QY 361 VPKKPSLTKRSRAQEQVPOAWTACTSSDSMAQPPOTETSTFRNQMPSTGTGSPG 420
DB 361 VPKKPSLTKRSRAQEQVPOAWTACTSSDSMAQPPOTETSTFRNQMPSTGTGSPG 420
QY 421 PRGNGAEROGMNSCRTPEDNPVTGRPLVNIYNGSGVGDNNYLTMOQTALPTMGLA 480
DB 421 PRGNGAEROGMNSCRTPEDNPVTGRPLVNIYNGSGVGDNNYLTMOQTALPTMGLA 480
QY 481 PSKNGRGLQHPPPVGSQBPDPKPAWSRPOGMNHSK 518
DB 481 PSKNGRGLQHPPPVGSQBPDPKPAWSRPOGMNHSK 518

RESULT 7

US-09-329-418-9
Sequence 9, Application US/09329418
Patent No. 6098539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 518
TYPE: PRP
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-9

Query Match 98.1%; Score 2722; DB 3; Length 518;
Best Local Similarity 99.0%; Pred. No. 2,8e-208;
Matches 513; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MSCVKLMPSCGAPALVSIIELENOELVGKDGCTVFRQHRKMGDYAVAKIVNSKASISRE 60
DB 1 MSCVKLMPSCGAPALVSIIELENOELVGKDGCTVFRQHRKMGDYAVAKIVNSKASISRE 60
QY 61 VKAASLSENEFVLRLEGVIERKVMNDOPKPAVLTAKFKMENGSLGILQSGCPRRPPLICRL 120
DB 61 VKAASLSENEFVLRLEGVIERKVMNDOPKPAVLTAKFKMENGSLGILQSGCPRRPPLICRL 120
QY 121 LKEVYLGMEFYLRHDOHPVTLHRDLKPSNVLPDELYHVKLADGSLTPGCGSGSGSGG 180
DB 121 LKEVYLGMEFYLRHDOHPVTLHRDLKPSNVLPDELYHVKLADGSLTPGCGSGSGSGG 180
QY 181 GTLGTLAPLPELVNVRKASTASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
DB 181 GTLGTLAPLPELVNVRKASTASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240

QY 241 SLAEIPQAGPETPGLGELKELMQLCWSSEPRKPSFOECLPKTDEVFOVEMNNNAVST 300
DB 241 SLAEIPQAGPETPGLGELKELMQLCWSSEPRKPSFOECLPKTDEVFOVEMNNNAVST 300
QY 301 VDFLSQLKSSNRRESIPESGCGGTENDGFRRTIENQHSRDVYVSEMLKLNLEPPSS 360
DB 301 VDFLSQLKSSNRRESIPESGCGGTENDGFRRTIENQHSRDVYVSEMLKLNLEPPSS 360
QY 361 VPKKPSLTKRSRAQEQVPOAWTACTSSDSMAQPPOTETSTFRNQMPSTGTGSPG 420
DB 361 VPKKPSLTKRSRAQEQVPOAWTACTSSDSMAQPPOTETSTFRNQMPSTGTGSPG 420
QY 421 PRGNGAEROGMNSCRTPEDNPVTGRPLVNIYNGSGVGDNNYLTMOQTALPTMGLA 480
DB 421 PRGNGAEROGMNSCRTPEDNPVTGRPLVNIYNGSGVGDNNYLTMOQTALPTMGLA 480
QY 481 PSKNGRGLQHPPPVGSQBPDPKPAWSRPOGMNHSK 518
DB 481 PSKNGRGLQHPPPVGSQBPDPKPAWSRPOGMNHSK 518

RESULT 8

US-09-531-914-9
Sequence 9, Application US/09531914
Patent No. 6267956
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/531,914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329,418
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 518
TYPE: PRP
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-9

Query Match 98.1%; Score 2722; DB 4; Length 518;
Best Local Similarity 99.0%; Pred. No. 2,8e-208;
Matches 513; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MSCVKLMPSCGAPALVSIIELENOELVGKDGCTVFRQHRKMGDYAVAKIVNSKASISRE 60
DB 1 MSCVKLMPSCGAPALVSIIELENOELVGKDGCTVFRQHRKMGDYAVAKIVNSKASISRE 60
QY 61 VKAASLSENEFVLRLEGVIERKVMNDOPKPAVLTAKFKMENGSLGILQSGCPRRPPLICRL 120
DB 61 VKAASLSENEFVLRLEGVIERKVMNDOPKPAVLTAKFKMENGSLGILQSGCPRRPPLICRL 120
QY 121 LKEVYLGMEFYLRHDOHPVTLHRDLKPSNVLPDELYHVKLADGSLTPGCGSGSGSGG 180
DB 121 LKEVYLGMEFYLRHDOHPVTLHRDLKPSNVLPDELYHVKLADGSLTPGCGSGSGSGG 180
QY 181 GTLGTLAPLPELVNVRKASTASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
DB 181 GTLGTLAPLPELVNVRKASTASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
QY 241 SLAEIPQAGPETPGLGELKELMQLCWSSEPRKPSFOECLPKTDEVFOVEMNNNAVST 300
DB 241 SLAEIPQAGPETPGLGELKELMQLCWSSEPRKPSFOECLPKTDEVFOVEMNNNAVST 300
QY 301 VDFLSQLKSSNRRESIPESGCGGTENDGFRRTIENQHSRDVYVSEMLKLNLEPPSS 360
DB 301 VDFLSQLKSSNRRESIPESGCGGTENDGFRRTIENQHSRDVYVSEMLKLNLEPPSS 360
QY 361 VPKKPSLTKRSRAQEQVPOAWTACTSSDSMAQPPOTETSTFRNQMPSTGTGSPG 420
DB 361 VPKKPSLTKRSRAQEQVPOAWTACTSSDSMAQPPOTETSTFRNQMPSTGTGSPG 420

QY 21 LENGLVKGDFGTFVPAORHKGVDYAVKIVSKAISREYKAMASLDNEFVLEGVIE 80
DB 1 LENGLVKGDFGTFVPAORHKGVDYAVKIVSKAISREYKAMASLDNEFVLEGVIE 60
QY 81 KVMNDOPKALVTKFENGSLGSLQSCPPRPMLLCRLKEVVLGKFFYLHDONPVLLH 140
DB 61 KVMNDOPKALVTKFENGSLGSLQSCPPRPMLLCRLKEVVLGKFFYLHDONPVLLH 120
QY 141 RDLKPSVNLDPDELHVLAADFGSLTFQGGSGSGTSGSGEPGCTIGYLADELFEVNNRKA 200
DB 121 RDLKPSVNLDPDELHVLAADFGSLTFQGGSGSGTSGSGEPGCTIGYLADELFEVNNRKA 180
QY 201 ASDVYSFGILMMNAVLAGREVELPTPEPSLYEAVCNONRNPISLAELPOAGPETPELEGLKE 260
DB 181 ASDVYSFGILMMNAVLAGREVELPTPEPSLYEAVCNONRNPISLAELPOAGPETPELEGLKE 240
QY 261 LMOLCMSSEPRDRPSFOECLP 281
DB 241 LMOLCMSSEPRDRPSFOECLP 261

RESULT 12
US-09-331-914-6
Sequence 6, Application US/09331914
Patent No. 6267956
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM 70536
CURRENT APPLICATION NUMBER: US/09/331,914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329,418
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 261
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Kinase Domain
US-09-331-914-6

Query Match 49.0%; Score 1358; DB 4; Length 261;
Best Local Similarity 99.2%; Pred. No. 2,4e-100;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 21 LENGLVKGDFGTFVPAORHKGVDYAVKIVSKAISREYKAMASLDNEFVLEGVIE 80
DB 1 LENGLVKGDFGTFVPAORHKGVDYAVKIVSKAISREYKAMASLDNEFVLEGVIE 60
QY 81 KVMNDOPKALVTKFENGSLGSLQSCPPRPMLLCRLKEVVLGKFFYLHDONPVLLH 140
DB 61 KVMNDOPKALVTKFENGSLGSLQSCPPRPMLLCRLKEVVLGKFFYLHDONPVLLH 120
QY 141 RDLKPSVNLDPDELHVLAADFGSLTFQGGSGSGTSGSGEPGCTIGYLADELFEVNNRKA 200
DB 121 RDLKPSVNLDPDELHVLAADFGSLTFQGGSGSGTSGSGEPGCTIGYLADELFEVNNRKA 180
QY 201 ASDVYSFGILMMNAVLAGREVELPTPEPSLYEAVCNONRNPISLAELPOAGPETPELEGLKE 260
DB 181 ASDVYSFGILMMNAVLAGREVELPTPEPSLYEAVCNONRNPISLAELPOAGPETPELEGLKE 240
QY 261 LMOLCMSSEPRDRPSFOECLP 281
DB 241 LMOLCMSSEPRDRPSFOECLP 261

RESULT 13
US-09-329-418-7
Sequence 7, Application US/09329418

Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM 70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 240
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Death Domain
US-09-329-418-7

Query Match 47.0%; Score 1305; DB 3; Length 240;
Best Local Similarity 99.6%; Pred. No. 3,4e-96;
Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 279 CLPKTDEVFOVNNNAAVSTVKDFLSQLKSSNRRFSIPESGGGTENDGFRRTIENOH 338
DB 1 CLPKTDEVFOVNNNAAVSTVKDFLSQLKSSNRRFSIPESGGGTENDGFRRTIENOH 60
QY 339 SRNDVYSEMLNKLNEEPSSVPRKCPSTLRSSAORBOVPOAWTACTSSDSMAOPPT 398
DB 61 SRNDVYSEMLNKLNEEPSSVPRKCPSTLRSSAORBOVPOAWTACTSSDSMAOPPT 120
QY 399 PETSTFRNQPSTSTGTPSPGRGNGAERGNMNSCTREPVPVYGRPLVINYKSGV 458
DB 121 PETSTFRNQPSTSTGTPSPGRGNGAERGNMNSCTREPVPVYGRPLVINYKSGV 180
QY 459 OYGDNNYLTMOQTALPTNGLAPSGKRGLOHPPVGSOSEPKPPEASRPOGMYNRSGK 518
DB 181 OYGDNNYLTMOQTALPTNGLAPSGKRGLOHPPVGSOSEPKPPEASRPOGMYNRSGK 240

RESULT 14
US-09-531-914-7
Sequence 7, Application US/09531914
Patent No. 6267956
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM 70536
CURRENT APPLICATION NUMBER: US/09/531,914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329,418
PRIOR FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 240
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Death Domain
US-09-531-914-7

Query Match 47.0%; Score 1305; DB 4; Length 240;
Best Local Similarity 99.6%; Pred. No. 3,4e-96;
Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 279 CLPKTDEVFOVNNNAAVSTVKDFLSQLKSSNRRFSIPESGGGTENDGFRRTIENOH 338
DB 1 CLPKTDEVFOVNNNAAVSTVKDFLSQLKSSNRRFSIPESGGGTENDGFRRTIENOH 60
QY 339 SRNDVYSEMLNKLNEEPSSVPRKCPSTLRSSAORBOVPOAWTACTSSDSMAOPPT 398
DB 61 SRNDVYSEMLNKLNEEPSSVPRKCPSTLRSSAORBOVPOAWTACTSSDSMAOPPT 120

QY 399 PETSTRNOMSPSTGTGPPSPGRNGOAEORGNNMSCTPEPPNYPYGRPLVNTYNSGV 438
DB 121 PETSTRNOMSPSTGTGPPSPGRNGOAEORGNNMSCTPEPPNYPYGRPLVNTYNSGV 180
QY 459 QVGDNNYITMOTTALTPTWGLAPSGKRGQLQHPPPVSGSGCKDEKDEANSRPQGYNHSR 518
DB 181 QVGDNNYITMOTTALTPTWGLAPSGKRGQLQHPPPVSGSGCKDEKDEANSRPQGYNHSR 240

RESULT 15

US-08-444-005-15

Sequence 15, Application us/08444005

Patent No 5674734

GENERAL INFORMATION:

APPLICANT: Leder, Philip

APPLICANT: Seed, Brian

APPLICANT: Stanger, Ben Z.

APPLICANT: Lee, Tae-Ho

APPLICANT: Kim, Emily

TITLE OF INVENTION: CELL DEATH PROTEIN

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street, Suite 3100

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,005

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,164

REFERENCE/DOCKET NUMBER: 00383/026001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

FAX: 200154

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 656 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-444-005-15

Query Match 15.1% Score 445.5; DB 1; Length 656;

Best Local Similarity 26.2% Pred. No. 2,3e-27;

Matches 158; Conservative 89; Mismatches 205; Indels 151; Gaps 23;

QY 15 LVSTEELEMDLVKDGSGFTVFRQRRKMGVDVAIVN-----SKAISREYKAMASL 67
DB 12 MASSDLLEKTL-DSGGFGKVSCLTIRSHGQFYLKRVYGPRAEYNEVLLECKMHRRL 70
QY 68 DNEFVLRLEG-VIEKVMDDOPKALVTYRKFNENGSISGLLOSQCRPMPPLCRLKREVL 126
DB 71 RRSRVYKLGIIIEGNY-----SLVMEYEMKGNLMHVKRQIDIVPLSLKGRIVPAIE 124
QY 127 GMFYLDQNPFLYLRDLKPSNYLPDELYKLAADGLSTFGGSGO-----SGT 174
DB 125 GNCYLDHG--VIRKDLKPERILVNDQFHKIADLGASFKTMSKLTREKDNKQREYSS 182
QY 175 GSGEGGTIGYLADELNVNRRKASTASDVSPGILMMAVLAGREVELPTEPSLYEAVC 234

DB 183 TKNNKGLITITMAEHLNDINAKPTKSDVYSGYIVAIIFAKRE---PYE-----NVIC 234
QY 235 NNO-----NRSLABLPOAGPETHPGLEKLMQLCWSEPKDRSF---QECLEPK 282
DB 235 TQPIYICIKSGRRPRVETILEYCPRE---IISLMERCWQAIPEDRPTFLGIEEPRPF 289
QY 283 TDEVF-QVVENNMAAVSTVADFLSOLKSNRRFS-----IPES----- 320
DB 290 YLSHFEEYEDY---ASLKEYPDQSPVLQRFESLQHDCEVLPFPSPRSNSDQPSLSSSQ 346
QY 321 --GCGTENDGPRRTIENGSRNDVYSENLK-----LNL 354
DB 347 GLQMGVPEESWSSSPETPDENDRSYQAKLQDEASTAFGLFAKQKTPPRKONEATNR 406
QY 355 EEPSPVPKCPSTLKRSRAQEOVPOAWTAG-----TSSDMAQPPQTPETST-FRNO 407
DB 407 EERKRKRVSHDPFAQQRAR---ENIKSAGARGSDPSTSRGLAVQQLSMPATQTVNNNG 463
QY 408 MSPSTGTSPSPGRNGOAEORGNNMSCTPEPPN-----PVTGRPLVN-----LY 453
DB 464 LYNQAGFTGTGYTPPNTLSQMTSTYKTPVETNLRGSTPTMPTFSGPVADDLKRTIF 523
QY 454 KSGYQVGDNNYITMOTTALTPTWGLAPSGKRGQLQHPPPVSGSGCKDEKDEANSRPQGY 513
DB 524 NSGIGIENHYMDV-----GLNSQPPNNTCK---EESTSRQQAIF 561
QY 514 NRS 516
DB 562 DNT 564

Search completed: August 13, 2002, 22:08:16
Job time: 3218 sec


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OY 1 MSCVKLMPGAPAPLVYSIBELNDELVGKDGFTGVFRAQHRKMGYDAVAVKIVNSKAISRE 60
DB 1 mscvklmpgagapaplvysibelelengelvgkdgftgvfraqhrkmgvdaavdkivnskaistre 60
OY 61 VKAMASIDNEFVRLRGVYERVNNDQPKRALYTRKFMENKSLGILLQSQCPRPVPLICRL 120
DB 61 vkamasidnefvlrlgvyekvnndqpkralytkfmenkslglilqsgcprrpvllicrl 120
OY 121 LKEVVLGMFTLNDQNPVLLHNDLKRPNVLPDELVHVLADFGSLTFQSGSGSGSGEPG 180
DB 121 lkevvlgmftlndqnpvllhndlkpsnvlpdpelvhvladfgsltfqsgsgsgsgsep 180
OY 181 GTTGAYLAPLFLVNNRKAISTADSVYSGILLMAVLAEREVELPTEPSLYLVAVCNKRNRP 240
DB 181 gttgylapelflvnnrkastadvysfgillmavlagrevelptepslylvavcnrnrp 240
OY 241 SLAELPQAGPEPTPGLGKELMQLCWSSEPRDRSPQECIPKTXDEYFQVNNNAVST 300
DB 241 slaelpqagpeptpgleglkelmqlcwsseprdrspqecipktxdevfqvnnmaavst 300
OY 301 VKDFLSQLKSSNRRESIPESGCGTEMDGFRRRTIENQSHNDVAVSEMLINKLNLPEPSS 360
DB 301 vkdfllsqllksnrresfipesgsgtcmdgfrtlienqshndvavsewlnklnlpepps 360
OY 361 VPKKCPSLTKRSRAQEDQVPAWTAAGTSSDSMAOPQPTPTSTFRNOMPSPTSTGTPSPG 420
DB 361 vpkcpsltktrsaqeqvpawtacgtsdsmaopqptptstfrnmpsptstgtpspg 420
OY 421 PRGNOAEROGKMNMSCRTPPEPNVTGRPLVNIYNCSGVOYGDNNVLTJMOOTLPTWGIA 480
DB 421 prngoaerogkmmnsctrppepnvtgrplvniyngsgvdygdnnvltmqotlptwgl 480
OY 481 PSCKGRGLQHPPPVSGQEGPKDPEAMSRPOGMVNHSGK 519
DB 481 psckgrglqhpprvsgqegpkdpeawsrpgqvmnhsgk 519

RESULT 3
AAB01524
ID AAB01524 standard; Protein: 518 AA.
XX
AC AAB01524;
XX
DB 08-NOV-2000 (first entry)
XX
DE Kinase of death (KOD).
XX
KW KOD: kinase of death; programmed cell death; apoptosis; cancer;
KW autoimmune disease; stroke; Alzheimer's disease; identification.
XX
OS Homo sapiens.
XX
PN US6096339-A.
XX
PD 01-AUG-2000.
XX
PF 10-JUN-1999; 99US-0329418.
XX
PR 10-JUN-1999; 99US-0329418.
XX
PA (GENE) ZENECA LTD.
XX
PI Gomes BC, Prosser JC, Kasof GM;
XX
DR WPI: 2000-523872/47.
XX
DR N-PSDB: AAA47701, AAA47702.
XX
PT New nucleic acids encoding a protein activator of apoptosis for
PT preventing, diagnosing and treating pathophysiological disorders
XX related to apoptosis
XX
PS Claim 1; Columns 33-36; 32pp; English.

```

```

XX The kinase of death (KOD) polypeptide is integral to the activation
CC process of cellular apoptosis (programmed cell death). Apoptosis is
CC needed to orchestrate biological maintenance of an organism during
CC development as well as to preserve the normal function and fitness of
CC tissues during a normal life span. Physiological conditions which
CC result from aberrant apoptosis may be dire. Cancer and autoimmune
CC disease may result when there is too little apoptosis as well as
CC severe stroke damage or the neurodegeneration of Alzheimer's disease
CC when there is too much apoptosis. The KOD polypeptide is useful for
CC studying pathophysiological disorders related to apoptosis as well
CC as for identifying compounds that modulate biological and/or
CC pharmacological activity of the native mediator of apoptosis.
XX
SQ Sequence 518 AA:
OY 1 MSCVKLMPGAPAPLVYSIBELNDELVGKDGFTGVFRAQHRKMGYDAVAVKIVNSKAISRE 60
DB 1 mscvklmpgagapaplvysibelelengelvgkdgftgvfraqhrkmgvdaavdkivnskaistre 60
OY 61 VKAMASIDNEFVRLRGVYERVNNDQPKRALYTRKFMENKSLGILLQSQCPRPVPLICRL 120
DB 61 vkamasidnefvlrlgvyekvnndqpkralytkfmenkslglilqsgcprrpvllicrl 120
OY 121 LKEVVLGMFTLNDQNPVLLHNDLKRPNVLPDELVHVLADFGSLTFQSGSGSGSGEPG 180
DB 121 lkevvlgmftlndqnpvllhndlkpsnvlpdpelvhvladfgsltfqsgsgsgsgsep 180
OY 181 GTTGAYLAPLFLVNNRKAISTADSVYSGILLMAVLAEREVELPTEPSLYLVAVCNKRNRP 240
DB 181 gttgylapelflvnnrkastadvysfgillmavlagrevelptepslylvavcnrnrp 240
OY 241 SLAELPQAGPEPTPGLGKELMQLCWSSEPRDRSPQECIPKTXDEYFQVNNNAVST 300
DB 241 slaelpqagpeptpgleglkelmqlcwsseprdrspqecipktxdevfqvnnmaavst 300
OY 301 VKDFLSQLKSSNRRESIPESGCGTEMDGFRRRTIENQSHNDVAVSEMLINKLNLPEPSS 360
DB 301 vkdfllsqllksnrresfipesgsgtcmdgfrtlienqshndvavsewlnklnlpepps 360
OY 361 VPKKCPSLTKRSRAQEDQVPAWTAAGTSSDSMAOPQPTPTSTFRNOMPSPTSTGTPSPG 420
DB 361 vpkcpsltktrsaqeqvpawtacgtsdsmaopqptptstfrnmpsptstgtpspg 420
OY 421 PRGNOAEROGKMNMSCRTPPEPNVTGRPLVNIYNCSGVOYGDNNVLTJMOOTLPTWGIA 480
DB 421 prngoaerogkmmnsctrppepnvtgrplvniyngsgvdygdnnvltmqotlptwgl 480
OY 481 PSCKGRGLQHPPPVSGQEGPKDPEAMSRPOGMVNHSGK 518
DB 481 psckgrglqhpprvsgqegpkdpeawsrpgqvmnhsgk 518

RESULT 4
AAE09430
ID AAE09430 standard; Protein: 518 AA.
XX
AC AAE09430;
XX
DB 19-NOV-2001 (first entry)
XX
DE Human kinase of death (KOD) protein activator of apoptosis.
XX
KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
XX cytosolic.
XX
OS Homo sapiens.
XX

```

FR	Key	Location/Qualifiers
FR	Domain	21..281
FT		/note="kinase domain"
FT	Misc-difference	83..85
FT		/note="Encoded by GCGCGCTCGAGC: This occurs while
FT	Misc-difference	112
FT		/note="Encoded by YGG: This occurs while decoding
FT		with AAd16313"
FT	Domain	280..518
FT		/note="Death domain"
XX	US6267956-B1.	
XX	31-JUL-2001.	
XX	21-MAR-2000; 2000DS-0531914.	
XX	10-JUN-1999; 99DS-0329418.	
XX	(ZENE) ZENECA LTD.	
XX	Gomes BC, Rasof GM, Prosser JC;	
XX	WPI: 2001-535022/59.	
XX	N-PSDB: AAD16312, AAD16313.	
XX	New human protein activator protein, useful for treating dysfunctional	
XX	apoptosis conditions and in screening assays to identify agonists which	
XX	agonize or mimic biological and/or pharmacological activity -	
XX	Claim 1; Column 33-36; 31pp; English.	
XX	The invention relates to human protein activator of apoptosis and	
XX	methods to identify compounds that modulate the biological and/or	
XX	pharmacological activity of the activator and hence regulate	
XX	apoptosis. The nucleic acid and amino acid sequences of the kinase	
XX	of death (KOD) are useful for identifying compounds that modulate	
XX	the biological and/or pharmacological activity of a native mediator	
XX	of apoptosis, for treating dysfunctional apoptosis conditions, in	
XX	screening assays to identify agonists which agonize or mimic	
XX	biological and/or pharmacological activity, induce production of or	
XX	prolong the biological half-life of the molecule in vivo or in vitro.	
XX	The present sequence is human KOD protein activator of apoptosis.	
XX	Sequence 518 AA:	

Query Match	99.18	Score 2750	DB 22	Length 518
Best Local Similarity	99.48	Fred. No. 2.1e-20		
Matches 515	Conservative 1	Mismatches 2	Indels 0	Gaps 0
QY	1	MSCVKLMPGAPAPLVASIEELNEQETVGKDFCTYFRAQHRKMGYDAVAKIVNSKAISRE	60	
Db	1	mscvklmpsgapaplvaisieelneqetvgkdfctyfraqhrkmgdyavaklvnskaistre	60	
QY	61	VKAASLDNNEFVLRBEVIEKVNMDDPKPAVYTKRMENGSLSGLQSCCPRPPLLCRL	120	
Db	61	vkamasldnefvlrbeviekvnmddppkpaavytkrmengsllsglqscprpplllcrl	120	
QY	121	LKEVYLGFVYHDOONPVLTLHRDLKPSNVLPPBELVHKTALADELSYFQGGSGSGSGSEEP	180	
Db	121	lkevylgfyhdoonpvltlhrdlkpsnvlppbelvhtkaladeslyfqqsgsgsgseep	180	
QY	181	GTGGLTAPLELVVNNKRAASTASDVYSFGILNNANVLAGEEVELPTBPSLVYDAVCONRRP	240	
Db	181	gttglylapelevnnnraastasdvyisfgilnnanvlagrevelptbpslvayavconrrp	240	
QY	241	SLASLPQAGEPTPGLKELKMLQALCSSSEPKRNPSTOECLPTDEDFQWYVNNNNAAVST	300	
Db	241	slaelpqageptpglelkelmlqalcsssepkrdptseclptddevfqwmnnnaavst	300	
QY	301	VKDELSQLKSNRRFSTIPESGGCGCTMDGFRRTIENQHSRNDVNVSEVLRNLNLEPPSS	360	

Db	301	vdflsqdisarrnrrifpsagsgstlmdgrrrtlenqhsnmwsewlnklnleppss	360
Oy	361	VRKCPSLTKRSRAQEEVPOAMTAGTSSDSMAQPPQPIETSTRNQMFSPSTGT7PSPG	420
Db	361	VPKKCPSLTKRSTRAGQGVPAQWLAGSSDSMAQPPQPIETSTRNQMFSPSTGT7PSPG	420
Oy	421	PRGNCGARCGGMNMSKRTPEEPNVTGAPLVNINVCSGVQGVQDNNTLTMQDTALPTMGIA	480
Db	421	prgnsgaerqgmwscrtpeepvtrgplvnlncsagvqgdmyltmqctcalptwja	480
Oy	481	PSGRGRLGHPVPVSGDQGPDPDPMANRQPGWYNISGR	518
Db	481	psgrkrglqhpvpvsgdqgpxkdpaeawtrpqgwynhsqk	518
RESULT 5			
AA01526			
ID	AA01526	standard; Protein: 518 AA.	
AC	AA01526;		
XX	08-NOV-2000	(first entry)	
XX			
DE	Kinase of death (KOD) dominant negative mutant.		
XX			
KW	KOD; kinase of death; programmed cell death; apoptosis; cancer;		
XX	autoimmune disease; stroke; Alzheimer's disease; identification.		
OS	Homo sapiens.		
PN	US6095539-A.		
PD	01-AUG-2000.		
PF	10-JUN-1999; 99US-0329418.		
XX			
PR	10-JUN-1999; 99US-0329418.		
PA	(ZENE) ZENECA LTD.		
XX			
PI	Gomes BC, Prosser JC, Kasof GM;		
DR	WPI; 2000-523872/47.		
PT	New nucleic acids encoding a protein activator of apoptosis for		
PT	preventing, diagnosing and treating pathophysiological disorders		
PT	related to apoptosis		
XX			
XX	Claim 5; Columns 37-40; 32pp; English.		
XX			
CC	The kinase of death (KOD) polypeptide is integral to the activation		
CC	process of cellular apoptosis (programmed cell death). Apoptosis is		
CC	needed to orchestrate biological maintenance of an organism during		
CC	development as well as to preserve the normal function and fitness of		
CC	cells during a normal life span. Physiological conditions which		
CC	result from aberrant apoptosis may be dire. Cancer and autoimmune		
CC	disease may result when there is too little apoptosis as well as		
CC	severe stroke damage or the neurodegeneration of Alzheimer's disease		
CC	when there is too much apoptosis. The KOD polypeptide is useful for		
CC	studying pathophysiological disorders related to apoptosis as well		
CC	as for identifying compounds that modulate biological and/or		
CC	pharmacological activity of the native mediator of apoptosis.		
CC	This KOD dominant negative mutant sequence differs from the wild		
CC	type KOD (AA01524) by having lysine at position 50 (ATP binding		
CC	site) replaced by arginine.		
XX			
XX	Sequence 518 AA:		

```
Query Match      99.0%  Score 2747;  DB 21;  Length 518;
Best local Similarity 99.2%  Pred. No. 3,56-206;
Matches 514;  Conservative 2;  Mismatches 2;  Indels 0;  Gaps 0;
```

```

OY 1 MSCVILMPGAPAPLVISIELENOELVGRDGFVFRQHRKMGDYAVKIVSKAISRE 60
DB 1 mscvilmppsgapaplviseelenqelvgkgfvtfrqhkmgdydvavilvnskaisre 60
OY 61 VKAASLIDNEFVLEBGEVIEKVMODDPKALVTFEMNGSLGLOSOCPRPMLICRL 120
DB 61 vkamslidnefvlebgviekvmddppalvtlcfmngslgllqgqcprrpmllicrl 120
OY 121 LKEVYLGMFVLDQNPVYLHRDLKPSNVLPDELVKTLADFGSLTFQGSQSCTGSGDEP 180
DB 121 lkevylgmfvldqnpvylhrdlkpsnvllpdelvkladfgslctfqsqsctgsgep 180
OY 181 GTLGVLAPELFVYNRRKASTASDVYSFGILMNAVLAGREVELPTPELSLYEAVCNRRONR 240
DB 181 gtlgvlapelfvynrrkastasdvysfgllmnavlagrevelptepelslyeaavcnrrnp 240
OY 241 SLAELPQAGPPTGEGIEKELMOLCWSSEPKRPSFOCLKRTDEVQVYENNNNAVST 300
DB 241 slaelpqagpptegeiekelmolcwssepkdrpsfoclkrtdeviqvnenmaavst 300
OY 301 VKDFLSQLKSSNRRFSLPESGOGCTEMDGFRTIENQSRNDVYSEMLKLNLEPPSS 360
DB 301 vkdfslsqkssnrrfslpesgogctemdgrftrienqsrndvymsewlnkleppss 360
OY 361 VPKKCPSLTRSRROEVOVQAWTACTSSDMAOPPORPSTFRNQMPSPTSTGRPSG 420
DB 361 vpkcpsltrsrroevovqawtagtssdsmaopporpstfrnqmppsptstgrpsg 420
OY 421 PRGNQGAEROGMNMSCRTPEPNVTGRPLVNTNCSGVQVGDNNYLTMOQTALPTWGLA 480
DB 421 prngngaerogmnmscrtpepnvtgrplvntncsgvqvgdnnyltmqctalptwgl 480
OY 481 PSKGKRGQLQHPYPVSGQEGPKDEPANSRPOGWYNHSGK 518
DB 481 pskgkrgqlqhppvsgqegpkdepaansrpgqwynhsgk 518

RESULT 6
AAE09432
ID AAE09432 standard; Protein: 518 AA.
AC AAE09432;
DT 19-NOV-2001 (first entry)
XX
DE Human kinase of death (KOD) dominant negative mutant, K50R.
XX
KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
KW cytosolic; mutant; muten.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6267956-B1.
XX
PD 31-JUL-2001.
XX
PE 21-MAR-2000; 2000US-0531914.
XX
PR 10-JUN-1999; 99US-0329418.
XX
PA (ZENNE ) ZENNECA LTD.
XX
PI Gomes BC, Kasof GM, Prosser JC;
XX
DR WPI; 2001-535022/59.
XX
PT New human protein activator protein, useful for treating dysfunctional
PT apoptosis conditions and in screening assays to identify agonists which
PT agonize or mimic biological and/or pharmacological activity -
XX
PS Disclosure: Column 37-40; 31pp; English.

```

```

XX The invention relates to human protein activator of apoptosis and
CC methods to identify compounds that modulate the biological and/or
CC pharmacological activity of the activator and hence regulate
CC apoptosis. The nucleic acid and amino acid sequences of the kinase
CC of death (KOD) are useful for identifying compounds that modulate
CC the biological and/or pharmacological activity of a native mediator
CC of apoptosis, for treating dysfunctional apoptosis conditions. In
CC screening assays to identify agonists which agonize or mimic
CC biological and/or pharmacological activity, induce production of or
CC prolong the biological half-life of the molecule in vivo or in vitro.
CC The present sequence is a dominant negative mutant of human KOD
CC protein activator of apoptosis. The lysine at position 50 of native
CC KOD is changed to arginine in the mutant sequence.
XX
SO Sequence 518 AA:

Query Match 99.0%; Score 2747; DB 22; Length 518;
Best Local Similarity 99.2%; Pred. No. 3,56-206;
Matches 514; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSCVILMPGAPAPLVISIELENOELVGRDGFVFRQHRKMGDYAVKIVSKAISRE 60
DB 1 mscvilmppsgapaplviseelenqelvgkgfvtfrqhkmgdydvavilvnskaisre 60
OY 61 VKAASLIDNEFVLEBGEVIEKVMODDPKALVTFEMNGSLGLOSOCPRPMLICRL 120
DB 61 vkamslidnefvlebgviekvmddppalvtlcfmngslgllqgqcprrpmllicrl 120
OY 121 LKEVYLGMFVLDQNPVYLHRDLKPSNVLPDELVKTLADFGSLTFQGSQSCTGSGDEP 180
DB 121 lkevylgmfvldqnpvylhrdlkpsnvllpdelvkladfgslctfqsqsctgsgep 180
OY 181 GTLGVLAPELFVYNRRKASTASDVYSFGILMNAVLAGREVELPTPELSLYEAVCNRRONR 240
DB 181 gtlgvlapelfvynrrkastasdvysfgllmnavlagrevelptepelslyeaavcnrrnp 240
OY 241 SLAELPQAGPPTGEGIEKELMOLCWSSEPKRPSFOCLKRTDEVQVYENNNNAVST 300
DB 241 slaelpqagpptegeiekelmolcwssepkdrpsfoclkrtdeviqvnenmaavst 300
OY 301 VKDFLSQLKSSNRRFSLPESGOGCTEMDGFRTIENQSRNDVYSEMLKLNLEPPSS 360
DB 301 vkdfslsqkssnrrfslpesgogctemdgrftrienqsrndvymsewlnkleppss 360
OY 361 VPKKCPSLTRSRROEVOVQAWTACTSSDMAOPPORPSTFRNQMPSPTSTGRPSG 420
DB 361 vpkcpsltrsrroevovqawtagtssdsmaopporpstfrnqmppsptstgrpsg 420
OY 421 PRGNQGAEROGMNMSCRTPEPNVTGRPLVNTNCSGVQVGDNNYLTMOQTALPTWGLA 480
DB 421 prngngaerogmnmscrtpepnvtgrplvntncsgvqvgdnnyltmqctalptwgl 480
OY 481 PSKGKRGQLQHPYPVSGQEGPKDEPANSRPOGWYNHSGK 518
DB 481 pskgkrgqlqhppvsgqegpkdepaansrpgqwynhsgk 518

RESULT 7
AAB01525
ID AAB01525 standard; Protein: 518 AA.
AC AAB01525;
DT 08-NOV-2000 (first entry)
XX
DE Kinase of death (KOD) dominant negative mutant.
XX
KW KOD; kinase of death; programmed cell death; apoptosis; cancer;
KW autoimmune disease; stroke; Alzheimer's disease; identification.
XX
OS Homo sapiens.

```

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XX  US6096539-A.
PN  01-ANG-2000.
XX  10-JUN-1999; 9905-0329418.
XX  10-JUN-1999; 9905-0329418.
XX  (ZENEC ) ZENEC A LTD.
PI  Comes BC, Prosser JC, Kasof GM;
XX  WPI: 2000-523872/47.
XX  New nucleic acids encoding a protein activator of apoptosis for
PT  preventing, diagnosing and treating pathophysiological disorders
PT  related to apoptosis
XX  Claim 5; Columns 35-38; 32pp; English.
XX  The kinase of death (KOD) polypeptide is integral to the activation
CC  process of cellular apoptosis (programmed cell death). Apoptosis is
CC  needed to orchestrate biological maintenance of an organism during
CC  development as well as to preserve the normal function and fitness of
CC  tissues during a normal life span. Physiological conditions which
CC  result from aberrant apoptosis may be dire. Cancer and autoimmune
CC  disease may result when there is too little apoptosis as well as
CC  severe stroke damage or the neurodegeneration of Alzheimer's disease
CC  when there is too much apoptosis. The KOD polypeptide is useful for
CC  studying pathophysiological disorders related to apoptosis as well
CC  as for identifying compounds that modulate biological and/or
CC  pharmacological activity of the native mediator of apoptosis.
CC  This KOD dominant negative mutant sequence differs from the wild
CC  type KOD (AAB01524) by having alanine at position 142 instead of
CC  aspartic acid.
XX  Sequence 518 AA:

Query Match      98.8%; Score 2742; DB 21; Length 518;
Best Local Similarity 99.2%; Pred. No. 8.7e-206;
Matches 514; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY  1 MSCVKLMPGAPAPLVISIELENOELVKGDFGVFAQHRKMGYDAVKIVNSKAISRE 60
DB  1 mscvklmpgagapaplvisleenogelvgkgdfgvfaqrkmgdyavavkivnskalsre 60
OY  61 VKAASLIDNEFVLRLEGVIERKVMQDPPKALVTKFENGSLSGILQSCPPMPULCRL 120
DB  61 vkamaelidnefvlrllegvlekvnmqdpkpalvtfkfnegslsgllsqcprmpulcrl 120
OY  121 LKRVVIGMFLYLDHONFVLIHRDLKPSNVLPPELHVKLADRGLESTPQSGSQSTGSGERG 180
DB  121 lkevvlgmflyldhnpvllhralkpsnyllpbelhvkldrglslcsgsgsgstgsgerg 180
OY  181 GTUGVLAPELVFNVNRKASTADVYSFGILMNAVLAGREVELPTPESLVEAVCNQKRRP 240
DB  181 gtclgylapelvfvnvrkasadsvysfgllmnavlagrevelelptepslvyeavcnqgnrp 240
OY  241 SLAELEPOAGPEPTGELGELKELMQLCMSSPEKDRPSFOCLPKTDEVRQVYENNNAAVST 300
DB  241 slaelelpagpeptgleglkelmqjlcwaseepdrpsfoecplktdevrfgvnenmaavst 300
OY  301 VKQFLQLQKASNRRESIFPSGOGGTEDMGFRRTIENQHSRNDVWVSMKLMLLEPPSS 360
DB  301 vkqflqlqkassnrresifpsgggtedmgfrrtlennqhsrindvwselinklnleppss 360
OY  361 VPKKCSLTKRSPAOEQQVQAAMTAGTSDSNAQPPQTPETSTFRNQMPSPSTCTPSPG 420
DB  361 vpkcksltkrspaoeqqvqaamtagtsdsnaqppqtpetstfrnqmpspstctgspspg 420
OY  421 PRGNQAGERGNMNSCRTPERPVPYGRPLVNTYNGSGVQVGDNNYLTLMQDTTALPTWGLA 480

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DB  421 prgnqagernmnsctrtpepnpvtygrplvntynsgvqvgdnnyltmqdtaltptwgl 480
OY  481 PSCKGRGLQHPPEPVYQSQEQKRPDPANSRPOGWYHNSKR 518
DB  481 psckgrglqhppepvysqeqkrdpdpansrpogwyhnskr 518

RESULT 8
AAE09431
ID  AAE09431 standard; Protein; 518 AA.
AC  AAE09431;
DT  19-NOV-2001 (first entry)
DE  Human kinase of death (KOD) dominant negative mutant, D143A.
XX  Human: protein activator; apoptosis; kinase of death; KOD; therapy;
XX  cytosolic; mutant; mutain.
XX  Homo sapiens.
OS  Synthetic.
XX  US6267956-B1.
XX  31-JUL-2001.
XX  21-MAR-2000; 2000US-0531914.
XX  10-JUN-1999; 9905-0329418.
PI  (ZENEC ) ZENEC A LTD.
XX  Comes BC, Kasof GM, Prosser JC;
XX  WPI: 2001-535022/59.
XX  New human protein activator protein, useful for treating dysfunctional
PT  apoptosis conditions and in screening assays to identify agonists which
PT  agonize or mimic biological and/or pharmacological activity -
XX  Example 8; Column 35-38; 31pp; English.
XX  The invention relates to human protein activator of apoptosis and
CC  methods to identify compounds that modulate the biological and/or
CC  pharmacological activity of the activator and hence regulate
CC  apoptosis. The nucleic acid and amino acid sequences of the kinase
CC  of death (KOD) are useful for identifying compounds that modulate
CC  the biological and/or pharmacological activity of a native mediator
CC  of apoptosis, for treating dysfunctional apoptosis conditions, in
CC  screening assays to identify agonists which agonize or mimic
CC  biological and/or pharmacological activity, induce production of or
CC  prolong the biological half-life of the molecule in vivo or in vitro.
CC  The present sequence is a dominant negative mutant of human KOD
CC  protein activator of apoptosis. The aspartic acid at position 143
CC  of native KOD is changed to alanine in the mutant sequence.
CC  Note: Column 11 of this specification describes that mutation occurs
CC  at position Asp143 of native KOD. But Asp is at position 142 in the
CC  native KOD sequence shown in sequence listing.
XX  Sequence 518 AA:

Query Match      98.8%; Score 2742; DB 22; Length 518;
Best Local Similarity 99.2%; Pred. No. 8.7e-206;
Matches 514; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY  1 MSCVKLMPGAPAPLVISIELENOELVKGDFGVFAQHRKMGYDAVKIVNSKAISRE 60
DB  1 mscvklmpgagapaplvisleenogelvgkgdfgvfaqrkmgdyavavkivnskalsre 60
OY  61 VKAASLIDNEFVLRLEGVIERKVMQDPPKALVTKFENGSLSGILQSCPPMPULCRL 120

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Db 61 VKAMASLDNEFVLRLEGVLEKWNWDQPKPALVCKFMENSLGSLIGSQCPRPVPLICRL 120
QY 121 LKEVVLGMFYLDHONPVLHRLDKPSNYLPPELHVKLADFGSLTFQSGSGSGSGEPG 180
Db 121 LKEVVLGMFYLDHONPVLHRLDKPSNYLPPELHVKLADFGSLTFQSGSGSGSGEPG 180
QY 181 GTGLAYLAPELFVNNKRASTASDVYSGFILMNAVLAGREVELPTEPSLYEAVCNQRNP 240
Db 181 GTGLAYLAPELFVNNKRASTASDVYSGFILMNAVLAGREVELPTEPSLYEAVCNQRNP 240
QY 241 SLAELPQAGPEPTGLGELKELMQLCMSSEPRDRPSFOCLPKTDEVFQVNNMNAAVST 300
Db 241 SLAELPQAGPEPTGLGELKELMQLCMSSEPRDRPSFOCLPKTDEVFQVNNMNAAVST 300
QY 301 VKDFLSQLKSNRFSIPESGGGTENQGFRTTENQHSNDVYSEMLTKLMLPEPPS 360
Db 301 VKDFLSQLKSNRFSIPESGGGTENQGFRTTENQHSNDVYSEMLTKLMLPEPPS 360
QY 361 VPKKCPSLTKRSRAQEDQYPOAWTNGTSSDMAOPPOTPETSTRNOMSPSTGTSPSG 420
Db 361 VPKKCPSLTKRSRAQEDQYPOAWTNGTSSDMAOPPOTPETSTRNOMSPSTGTSPSG 420
QY 421 PRGNQGAERGMNMSCRTPEPNVGRPLVNIYNGSGVOGDNNYLTMOOT7ALPTMGLA 480
Db 421 PRGNQGAERGMNMSCRTPEPNVGRPLVNIYNGSGVOGDNNYLTMOOT7ALPTMGLA 480
QY 481 PSCKGRGLQHPVPVSGOEGPKDPEASRPQGWYHNSGK 518
Db 481 PSCKGRGLQHPVPVSGOEGPKDPEASRPQGWYHNSGK 518

RESULT 9
AAB01530 standard: Protein: 518 AA.
ID AAB01530:
AC AAB01530:
XX 08-NOV-2000 (first entry)
XX 08-NOV-2000 (first entry)
DE Kinase of death (KOD) dominant negative mutant.
XX KOD, kinase of death, programmed cell death, apoptosis; cancer;
XX autoimmune disease; stroke; Alzheimer's disease; identification.
XX Homo sapiens.
XX US6096539-A.
XX 01-AUG-2000.
XX 10-JUN-1999: 990US-0329418.
XX 10-JUN-1999: 990US-0329418.
XX (ZENNE ) ZENNECA LTD.
XX Gomes BC, Prosser JC, Kasof GM:
XX WPL: 2000-523872/47.
XX
XX New nucleic acids encoding a protein activator of apoptosis for
XX preventing, diagnosing and treating pathophysiological disorders
XX related to apoptosis
XX
XX C1a1m 5; Columns 45-48; 32pp: English.
XX
XX The kinase of death (KOD) polypeptide is integral to the activation
XX process of cellular apoptosis (programmed cell death). Apoptosis is
XX needed to orchestrate biological maintenance of an organism during
XX development as well as to preserve the normal function and fitness of
XX tissues during a normal life span. Physiological conditions which
XX result from aberrant apoptosis may be dire. Cancer and autoimmune

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CC disease may result when there is too little apoptosis as well as
CC severe stroke damage or the neurodegeneration of Alzheimer's disease
CC when there is too much apoptosis. The KOD polypeptide is useful for
CC studying pathophysiological disorders related to apoptosis as well
CC as for identifying compounds that modulate biological and/or
CC pharmacological activity of the native mediator of apoptosis.
CC This KOD dominant negative mutant sequence differs from the wild
CC type KOD (AAB01524) by having both tryptophan residues at positions
CC 435 and 478 replaced by alanine.
CC
SQ Sequence 518 AA:
Query Match 98.1%; Score 2722; DB 21; Length 518;
Best Local Similarity 99.0%; Pred. No. 3,26-204;
Matches 513; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MSCRTKLPSSGAPRPLVSIETLENQELVGGKGGTYFRARHKKRYDVAIVYNSKATSE 60
Db 1 MSCRTKLPSSGAPRPLVSIETLENQELVGGKGGTYFRARHKKRYDVAIVYNSKATSE 60
QY 61 VKAMASLDNEFVLRLEGVLEKWNWDQPKPALVCKFMENSLGSLIGSQCPRPVPLICRL 120
Db 61 VKAMASLDNEFVLRLEGVLEKWNWDQPKPALVCKFMENSLGSLIGSQCPRPVPLICRL 120
QY 121 LKEVVLGMFYLDHONPVLHRLDKPSNYLPPELHVKLADFGSLTFQSGSGSGSGEPG 180
Db 121 LKEVVLGMFYLDHONPVLHRLDKPSNYLPPELHVKLADFGSLTFQSGSGSGSGEPG 180
QY 181 GTGLAYLAPELFVNNKRASTASDVYSGFILMNAVLAGREVELPTEPSLYEAVCNQRNP 240
Db 181 GTGLAYLAPELFVNNKRASTASDVYSGFILMNAVLAGREVELPTEPSLYEAVCNQRNP 240
QY 241 SLAELPQAGPEPTGLGELKELMQLCMSSEPRDRPSFOCLPKTDEVFQVNNMNAAVST 300
Db 241 SLAELPQAGPEPTGLGELKELMQLCMSSEPRDRPSFOCLPKTDEVFQVNNMNAAVST 300
QY 301 VKDFLSQLKSNRFSIPESGGGTENQGFRTTENQHSNDVYSEMLTKLMLPEPPS 360
Db 301 VKDFLSQLKSNRFSIPESGGGTENQGFRTTENQHSNDVYSEMLTKLMLPEPPS 360
QY 361 VPKKCPSLTKRSRAQEDQYPOAWTNGTSSDMAOPPOTPETSTRNOMSPSTGTSPSG 420
Db 361 VPKKCPSLTKRSRAQEDQYPOAWTNGTSSDMAOPPOTPETSTRNOMSPSTGTSPSG 420
QY 421 PRGNQGAERGMNMSCRTPEPNVGRPLVNIYNGSGVOGDNNYLTMOOT7ALPTMGLA 480
Db 421 PRGNQGAERGMNMSCRTPEPNVGRPLVNIYNGSGVOGDNNYLTMOOT7ALPTMGLA 480
QY 481 PSCKGRGLQHPVPVSGOEGPKDPEASRPQGWYHNSGK 518
Db 481 PSCKGRGLQHPVPVSGOEGPKDPEASRPQGWYHNSGK 518

RESULT 10
AAE09436 standard: Protein: 518 AA.
ID AAE09436:
AC AAE09436:
XX 19-NOV-2001 (first entry)
XX 19-NOV-2001 (first entry)
DE Human kinase of death (KOD) dominant negative mutant, W435A/W478A.
XX Human kinase of death (KOD) dominant negative mutant, W435A/W478A.
XX Human; protein activator; apoptosis; kinase of death; KOD; therapy;
XX cytosolic; mutant; mutain.
XX
XX Homo sapiens.
XX Synthetic.
XX US6267956-B1.
XX 31-JUL-2001.
XX

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XX 21-MAR-2000; 2000US-0531914.
 PF 10-JUN-1999; 99US-0329418.
 XX (ZENE) ZENECA LTD.
 XX Gomez BC, Kasof GM, Prosser JC;
 XX WPI: 2001-535022/59.
 DR New human protein activator protein, useful for treating dysfunctional
 XX apoptosis conditions and in screening assays to identify agonists which
 PT agonize or mimic biological and/or pharmacological activity -
 XX
 PS Disclosure: Column 45-48; 31pp; English.
 CC The invention relates to human protein activator of apoptosis and
 CC methods to identify compounds that modulate the biological and/or
 CC pharmacological activity of the activator and hence regulate
 CC apoptosis. The nucleic acid and amino acid sequences of the kinase
 CC of death (KOD) are useful for identifying compounds that modulate
 CC the biological and/or pharmacological activity of a native mediator
 CC of apoptosis, for treating dysfunctional apoptosis conditions, in
 CC screening assays to identify agonists which agonise or mimic
 CC biological and/or pharmacological activity, induce production of or
 CC prolong the biological half-life of the molecule in vivo or in vitro.
 CC The present sequence is a dominant negative mutant of human KOD
 CC and 478 of native KOD are changed to alanine in the mutant sequence.
 CC Note: Column 12 of this specification describes that mutation occurs
 CC at positions Trp435 and Trp478 of native KOD. But Trp are at positions
 CC 434 and 477 in the native KOD sequence shown in sequence listing.
 XX
 SQ Sequence 518 AA:
 Query Match 98.1%; Score 2723; DB 22; Length 518;
 Best Local Similarity 99.0%; Pred. No. 3.2e-204;
 Matches 513; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MSCVKLMPGAPAPLVSTIEENDELVKDGFVPAQRKKGVDVAVYNSKAISRE 60
 DB 1 mscvklmpgapaaplvsstieenlenglvkggfgfvtqqrktkydvavynskaisre 60
 QY 61 VKAMSLDNEPVLRLGCVTEYVNMDDPKRALYKRMENSGSLGLQSCPPRMLLCRL 120
 DB 61 vkamsldepfvrllegvteyevnmddpkralvkrmenstgslglqscpprmplicrl 120
 QY 121 LKEVYLGKCYLHDQNPVLIHDLKPSNYLPPELHVKLADFGSLTFGGSGSGSGERG 180
 DB 121 lkevyigmfylvhdqnpvllhcdlkpsnvlldpelnhvkldfsltfggsgsgsgsepg 180
 QY 181 GTLGAYLAPELFVNVRKASTASDVYSEFGLIMAVLAGREVELPTEPSLYEAVCNRNRP 240
 DB 181 gtlgylapelfvvnvrkastadvsyfgllmavlagrevelptepealyeavcnrnp 240
 QY 241 SLAELDPAQPEPGLGKLELMQCKHSEPRDRSPQECPLKTDVDFQVYENNNANAYST 300
 DB 241 slaelpaqpepglegklemqckhseprdrspqecplktdvdfqvennnamaavst 300
 QY 301 VQDFLSQLKSNRRRPSIPESGOGTEMDGFRRTIENHSHNDVAVSEMLNKLLEPPSS 360
 DB 301 vqdfllsqllksnrpsipesgggtendgfrttenhshndvavsemlnklleppss 360
 QY 361 VPKKPSLTKRSRAQEDQVPOAMTACTSSDSMAOPQPTPTSEFRNOMSPSTGTPSPG 420
 DB 361 vpkpsslktrsaqeqdvpoamtactssdsmaopqptptsefrnomspsstgtpspg 420
 QY 421 PRGNGAENQGNNSGCRPERNPVTGRPLVNIYNGSGVQGVDDNNYLYMQQTALPTMGLA 480
 DB 421 prngnaenqgnnsqcrpernpvtgrplvniyngsgvqgvddnnylymqqtaltptmgl 480
 DB 421 prngnaenqgnnsqcrpernpvtgrplvniyngsgvqgvddnnylymqqtaltptmgl 480

QY 481 PSQKRGLOHPPVSGSGEGRKDEPMSRPOGWNHSGK 518
 DB 481 psqkrglohppvsgsggegrkdepmssrpgwnhsgk 518
 RESULT 11
 AAB6604
 ID AAB6604 standard; protein; 497 AA.
 XX
 AC AAB6604;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human h15590 protein.
 XX
 KW Human; protein kinase; cell growth; tumour; cancer; immune;
 XX Inflammatory; respiratory; haematological; bone disorder.
 OS Homo sapiens.
 XX
 PN W0200100879-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000MO-US18291.
 XX
 PR 30-JUN-1999; 99US-0345473.
 XX
 PR 01-MAY-2000; 2000US-0562480.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Hodge MR, Meyers R, Williamson M;
 DR WPI: 2001-061977/07.
 XX
 PT New protein kinase polypeptides, nucleic acids and anti-kinase
 PT antibodies, useful for diagnosing and treating e.g. cancer,
 PT Inflammatory, immune, cardiovascular and bone disorders -
 XX
 PS Claim 1: Fig 10; 93pp; English.
 XX
 CC The present invention relates to human protein kinase. The proteins
 CC are from new human genes termed h12832, h14338, h14833, h15990,
 CC h15993, h16541 and h2252. The proteins may be used to identify
 CC modulators of their activity. The proteins may also be used to derive
 CC products for the treatment of cellular growth related disorders,
 CC malignancies, cancers, immune, inflammatory, respiratory,
 CC haematological and bone-related disorders.
 XX
 SQ Sequence 497 AA:
 Query Match 95.1%; Score 2639; DB 22; Length 497;
 Best Local Similarity 99.4%; Pred. No. 9.2e-198;
 Matches 494; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 22 ENDELVKDGFVTPRAQRKNGIDVAVKIVNSAISREYKAMASLDNEPVLRLGCVTE 81
 DB 22 endelvkgdgvtpraqrkngidvavkivnsaisrevkamaasldnepfvrllegvte 81
 QY 81 ENGELVYKSGYGFVTFQGRKTVGYDVAVKIVNSKASIREVKAMASLDNEPVLRLGCVTE 141
 DB 81 engelyvkgsgygfvtfqgrktvgydvavkivnskaisrevkamaasldnepfvrllegv 141
 QY 142 DLRKSNVLPPELHVKLADFGSLTFGGSGSGSGERGCTGLAYLAPELFVNVRKASTA 201
 DB 142 dlrsnvlppeelnhvkldfsltfggsgsgsgsepgctglaylapelfvvnvrkast 201
 QY 201 VQDFLSQLKSNRRRPSIPESGOGTEMDGFRRTIENHSHNDVAVSEMLNKLLEPPSS 261
 DB 201 vqdfllsqllksnrpsipesgggtendgfrttenhshndvavsemlnklleppss 261
 QY 261 VPKKPSLTKRSRAQEDQVPOAMTACTSSDSMAOPQPTPTSEFRNOMSPSTGTPSPG 321
 DB 261 vpkpsslktrsaqeqdvpoamtactssdsmaopqptptsefrnomspsstgtpspg 321
 DB 261 vpkpsslktrsaqeqdvpoamtactssdsmaopqptptsefrnomspsstgtpspg 321

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Db 241 mqlwseppdrpsfgeclpkddevfqlmvenmmaaavetvdfisqrlrrsnrtfslpesg 300
Oy 322 OGGETMDGFRRIIENQHSRNDVYSEWLNLKLEPPSSVPKPKPSLTNKSRAOEQVQ 381
Db 301 qggfemgffrrclenqlsrndwvsewlnklnleppsvpkckpsltkrsgaeqvpq 360
Oy 382 AWTAGTSSDAMAPQPTPERTSPFRNOMPSPTGTPSPGPGNGAROGNMSCHTEPP 441
Db 361 awtsgtsdamaqpptpertsfrngmpscscgcpspgpgngarqgmavscrtpep 420
Oy 442 NPVTGRPLVNYKCSGVQVGDNNYLTMOQTALPTWGLAPSGKRGIQHPVYGOEGPK 501
Db 421 npvtgrplvnykncsvqvdnnyltmqqtalptwglapsgkrgiqhpbppvsgsqp 480
Oy 502 DPEAMSRPOGMVNRSGK 518
Db 481 dpeawsrpgvnyhsgk 497

RESULT 12
AB18658
ID AB18658 standard; Protein: 485 AA.
XX
AC AB18658;
XX
DT 22-JAN-2001 (first entry)
XX
DE A human regulator of intracellular phosphorylation.
XX
KW Human; intracellular phosphorylation regulator; HRIP; stroke; myeloma;
KW neurological disorder; Parkinson's disease; demyelinating disease;
KW meningitis; developmental disorder; neuromuscular disorder; cancer;
KW myasthenia gravis; cell proliferative disorder; actinic keratosis;
KW arteriosclerosis; leukemias; melanoma; bronchitis;
KW autoimmune disorder; inflammatory disorder; Addison's disease;
KW acquired immunodeficiency disease; allergy; diabetes mellitus;
KW rheumatoid arthritis; microbial infection; trauma.
XX
OS Homo sapiens.
XX
FX Key Location/Qualifiers
FX Modified-site 16
FX Domain /note- "potential phosphorylation site"
FX Modified-site 26..247
FX Modified-site /note- "eukaryotic protein kinase domain"
FX Active-site 66
FX /note- "potential glycosylation site"
FX 105..117
FX Modified-site /note- "protein kinase catalytic site"
FX 166
FX Modified-site /note- "potential phosphorylation site"
FX 167
FX Modified-site /note- "potential phosphorylation site"
FX 208
FX Modified-site /note- "potential phosphorylation site"
FX 242
FX Modified-site /note- "potential phosphorylation site"
FX 267
FX Modified-site /note- "potential phosphorylation site"
FX 278
FX Modified-site /note- "potential phosphorylation site"
FX 283
FX Modified-site /note- "potential phosphorylation site"
FX 283
FX Modified-site /note- "potential phosphorylation site"
FX 292
FX Modified-site /note- "potential phosphorylation site"
FX 306
FX Modified-site /note- "potential phosphorylation site"
FX 336
FX Modified-site /note- "potential phosphorylation site"
FX 354
FX Modified-site /note- "potential phosphorylation site"

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FT Modified-site /note- "potential phosphorylation site"
FT 370
FT /note- "potential phosphorylation site"
FT 400
FT Modified-site /note- "potential glycosylation site"
FT 402
FT Modified-site /note- "potential phosphorylation site"
FT 412
FT Modified-site /note- "potential phosphorylation site"
FT 421
FT Modified-site /note- "potential glycosylation site"
FT 449
FT Modified-site /note- "potential phosphorylation site"
FT 481
FT Modified-site /note- "potential glycosylation site"
FT 483
FT Modified-site /note- "potential phosphorylation site"
FT /note- "potential phosphorylation site"
PN W0200055332-A2.
XX
PD 21-SEP-2000.
XX
PD 17-MAR-2000; 2000MO-DS07277.
XX
PR 18-MAR-1999; 99US-0125593.
PR 20-MAY-1999; 99US-0135049.
PR 09-JUL-1999; 99US-0143188.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Tang YT, Yue H, Hillman JT, Baughn MR, Azimzai Y;
PI Lu DW, Au-Young J;
XX
DR WPI: 2000-602121/57.
XX
DR N-PSDB: AAA75675.
XX
PT Novel human intracellular phosphorylation regulator polypeptides and
PT polynucleotides for diagnosis, prevention and treatment of
PT neurological, cell proliferative and autoimmune/inflammatory disorders
PT -
XX
PS Claim 1: Page 76-77; 96pp; English.
XX
CC The present sequence represents a human regulator of intracellular
CC phosphorylation (HRIP). HRIP is useful for screening agonists and
CC antagonists of HRIP polypeptide. HRIP and its agonist or antagonist
CC are useful for treating a disease or condition associated with
CC decreased or increased expression of functional HRIP. Diseases treated
CC or diagnosed include neurological disorders such as stroke, Parkinson's
CC disease, demyelinating diseases, bacterial and viral meningitis and
CC other developmental disorders of the central nervous system,
CC neuromuscular disorders, myasthenia gravis, cell proliferative disorders
CC such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer
CC including leukemia, melanoma, myeloma and cancer of the adrenal gland,
CC bladder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/
CC inflammatory disorder such as Addison's disease, acquired
CC immunodeficiency diseases, allergies, bronchitis, diabetes mellitus,
CC rheumatoid arthritis, microbial infection and trauma.
XX
SQ Sequence 485 AA:

Query Match 89.0%; Score 2470; DB 21; Length 485;
Best Local Similarity 99.6%; Pred. No. 1,46-184;
Matches 462; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 55 KAISREYKAAASLDNFEVLTLEGVYKVMDDPPKALVTKFNKNGSISGLDSQCFRPP 114
Db 22 kaisrevkamaasldnfevltlegvlykvmddppkpalvtkfmgngslsllsqcprpw 81
Oy 115 PLICRLAKFVYLKMFYILHONPVLHRODKPSNVLPPELVNLTADRGSLTFCGGSOSGT 174
Db 82 plicrlakfvyllkmfyilhonpvlhrodkpsnvlppelevnltadrgsltfcggsosgt 141

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OY 175 GSGEPGIGTGLAPLPELVNVRKASTASDVSTSGILMAVLAGREVLPTEPSLYEAVC 234
DB 142 GSEPPGTLGYLAPLPELVNVRKASTASDVSTSGILMAVLAGREVLPTEPSLYEAVC 201
OY 235 NQNRSLAELEQAGPERPGLGELKELNQLQMSSEPPDRSPFQECLEPTDEVFOYENNM 294
DB 202 nqnrslaelpqagperpglegleklnqlqmsseppdrspfqecleptdevfoynnm 261
OY 295 NNAVSVKRFSLQSLSSNRFSIPESGCGTENDGFRRTIENHSDNDVNSFNKLNL 354
DB 262 nnavsvkrfslqslssnrfsipesgcgtenmgfrttiendhndvnsfnklnl 321
OY 355 EEPSSVPRKCPSTLRKSHAOEYVQAMTAGTSSDMAOPQPTETSTFRNQMPSPTST 414
DB 322 eepssvprkcpstlrkshaoeyvqamtagtssdmaopqptetstfrnqmpstst 381
OY 415 GPPSPRQNGABRQGMMSGRTPEPNTYGRPLVNIYNGSGVQYQDNNYLTMOQTAL 474
DB 382 gppsprngabrqgmmsgtrtpepntygrplvniyngsgvqyqdnnyltmqqtal 441
OY 475 PRMGLAPSGKGLQHPVYVSGQEGPRKPMASRPQGMVNRSGK 518
DB 442 prmglapsgkglqhpvyvsgqegprkpmasrpggmvrsgk 485

RESULT 13
AAV45047
ID AAV45047 standard; Protein: 437 AA.
AC AAV45047;
XX
DT 31-MAY-2000 (first entry)
DE Human Apop3 (82-518) truncation mutant.
XX
KW Apop3 truncation mutant; Apop3 protein; apoptotic protein; cytostatic;
KW immunotherapy; RIP3; receptor-interacting protein; apoptosis modulation;
KW apoptosis-mediated disorder; TNFalpha-induced caspase activation;
KW cancer; autoimmune disorder; cytostatic; degenerative disorder;
KW viral infection; cell loss; inhibitor of apoptosis protein; IAP;
KW TNFalpha signalling complex; tumour necrosis factor.
XX
OS Homo sapiens.
XX
PN WO200007545-A2.
XX
PD 17-FEB-2000.
XX
PE 06-AUG-1999; 99MO-US17776.
XX
PR 06-AUG-1998; 98US-0095587.
PR 06-AUG-1998; 98US-0095590.
PR 08-SEP-1998; 98US-0099486.
XX
PA (RIGEL-) RIGEL PHARM INC.
XX
PI Luo Y, Huang BC, Shen M, Yu PW;
XX
DR WPI; 2000-205547/18.
XX
PT Novel apoptotic proteins Apop1, Apop2 and Apop3 and recombinant nucleic
PT acids encoding them for use in screening modulators which is useful for
PT diagnosis and treatment of diseases
XX
PS Example 2; Page: 64pp; English.
XX
CC The patent discloses the use of novel apoptotic proteins and related
CC molecules involved in apoptosis modulation. Expression vectors
CC comprising the Apop DNA can be used to transform host cells. Apop DNA
CC can be administered as DNA vaccines. Apop proteins are used to make
CC polyclonal and monoclonal antibodies for use in immunotherapy. The
CC proteins are useful in treating apoptosis-mediated disorders including

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CC cancer, autoimmune disorders, sustained viral infection, inappropriate
CC cell loss and degenerative disorders. Drug candidates that affect Apop
CC bioactivity are identified by screening. The present sequence is a
CC truncation mutant of Apop3 (82-518) protein, also known as RIP3
CC (receptor-interacting protein). This was used in experiments to
CC demonstrate activation of cellular caspases and NF kappaB (nuclear
CC factor kappaB). This N-terminal deletion mutant was able to activate
CC caspase activity and induced higher luciferase activity than full length
CC Apop3. The results indicated that Apop3's kinase activity is not
CC required for caspase activation. NF kappa B activation and cell death.
CC NOTE: The present sequence is not given in the specification but is
CC derived from Apop3 protein (AAV45042).
XX
SQ Sequence 437 AA;
XX
Query Match 85.0%; Score 2357; DB 21; Length 437;
Best Local Similarity 100.0%; Pred. No. 8,4e-176;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 82 VNMOPDRPALYTRFENSGISGLQSCPRPWPLICRLKEVLMFYLHNPVILHR 141
DB 1 VNMOPDRPALYTRFENSGISGLQSCPRPWPLICRLKEVLMFYLHNPVILHR 60
OY 142 DLKPSNVLPPPELVNVRKASTASDVSTSGILMAVLAGREVLPTEPSLYEAVC 201
DB 61 dlkpsnvlpppelevnvrkastasdvsstsgilmaavlagerelpetpslyeavncasta 120
OY 202 SDVSTSGILMAVLAGREVLPTEPSLYEAVCNRNRPDLAPQAGPTEPGLGREL 261
DB 121 sdvstsgilmaavlagerelpetpslyeavncnrnpdlapagptepglglel 180
OY 262 MQLCMSSEPPDRSPFQECLEPTDEVFOYENNMNAVSTKDFLSKSNRFSIPESG 321
DB 181 mqlcmsseppdrspfqecleptdevfoynnmnavstkdflsksnrfsipesg 240
OY 322 QCGTENDGFRRTIENHSDNDVNSFNKLNLSEPPSVPRKCPSTLRKSHAOEYVQ 381
DB 241 qcgtenmgfrttiendhndvnsfnklnlseppsvprkcpstlrkshaoeyvpq 300
OY 382 AMTAGTSSDMAOPQPTETSTFRNQMPSPTSTGTPSPGRQGMMSGRTPEP 441
DB 301 amtagtssdmaopqptetstfrnqmpststgtpspgrqgmmsgtrtpep 360
OY 442 NPVTGRPLVNIYNGSGVQYQDNNYLTMOQTALPTWGLAPSGKGLQHPVYVSGQ 501
DB 361 npvtgrplvniyngsgvqydnnyltmqqtalptwglapsgkglqhpvyvsgqgpx 420
OY 502 DPEASRPQGMVNRSGK 518
DB 421 dpeasrpggmvrsgk 437

RESULT 14
AAV45043
ID AAV45043 standard; Protein: 436 AA.
XX
AC AAV45043;
XX
DT 31-MAY-2000 (first entry)
DE Human Apop3 (1-436) C-terminal truncation mutant.
XX
KW Apop3 truncation mutant; Apop3 protein; apoptotic protein; cytostatic;
KW immunotherapy; RIP3; receptor-interacting protein; apoptosis modulation;
KW apoptosis-mediated disorder; TNFalpha-induced caspase activation;
KW cancer; autoimmune disorder; cytostatic; degenerative disorder;
KW viral infection; cell loss; inhibitor of apoptosis protein; IAP;
KW TNFalpha signalling complex; tumour necrosis factor.
XX
OS Homo sapiens.
XX
PI Key Location/Qualifiers

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FT Domain 1..274 /note= "homologous to kinase domain of RIP"
PT 21..287 /label= kinase_domain
FT /note= "478 homologous to RIP kinase domain and 428
FT homologous to RIP2/RICK/CARDIAC kinase domain"
PN MO200007545-A2.
XX 17-FEB-2000.
XX
XX 06-AUG-1999; 99MO-0517776.
XX
XX 06-AUG-1998; 98US-0095587.
XX 06-AUG-1998; 98US-0095590.
XX 08-SEP-1998; 98US-0099486.
XX
XX (RICE-) RICE PHARM INC.
XX
XX Luo Y, Huang BCB, Shen M, Yu FW;
XX
XX WPI: 2000-205547/18.
XX
XX Novel apoptotic proteins Apopt1, Apopt2 and Apopt3 and recombinant nucleic
XX acids encoding them for use in screening modulators which is useful for
XX diagnosis and treatment of diseases -
XX
XX Example 2; Page-; 64pp; English.
XX
XX The patent discloses the use of novel apoptotic proteins and related
XX molecules involved in apoptosis modulation. Expression vectors
XX comprising the Apop DNA can be used to transform host cells. Apop DNA
XX can be administered as DNA vaccines. Apop proteins are used to make
XX polyclonal and monoclonal antibodies for use in immunotherapy. The
XX proteins are useful in treating apoptosis-mediated disorders including
XX cancer, autoimmune disorders, sustained viral infection, inappropriate
XX cell loss and degenerative disorders. Drug candidates that affect Apop
XX bioactivity are identified by screening. The present sequence is a
XX C-terminal truncation mutant of Apopt3 (1-436) protein also known as
XX RIP3 (receptor-interacting protein). This mutant has dramatically
XX reduced binding affinity for RIP and fails to induce apoptosis.
XX Apopt3 (1-436) inhibited TNFalpha-induced caspase activation. Apopt3 is
XX associated with the TNFalpha (tumour necrosis factor) signalling complex
XX and TNF induced NF (nuclear factor) kappaB transcription factor
XX activation.
XX Note: The present sequence is not given in the specification but is
XX derived from Apopt3 protein (AAV45042).
XX
XX Sequence 436 AA;

```

Query Match 83.0%; Score 2302; DB 21; Length 436;
 Best Local Similarity 100.0%; Pred. No. 1.7e-171;
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSCYKLPSCAPAPLIVSIEELNQELVGDGCVFRAQHRKMDYAVKIVSKAISRE 60
DB 1 mscyklvpasgaplpvslaelnqelvgdgcvtfrqhrkmdyavavivskaisre 60
QY 61 VKAAASLDNEFVLRIGCVTEKVMODPKRAYTKFMKNGSLSLDSCPRWPLICLU 120
DB 61 vkmaasldnefvlrlegvtekvmodpkralvtfkmngslslslsqprwplliclu 120
QY 121 LKEVYLAQETLHNDONPVLHRLDKPSNVLPDELIVKLADFGISTFGGSGSGSGERG 180
DB 121 lkevyigmfylvhndqnpvllhrdlkpsnvlpdelivkladfgistfggsqsgsgsrg 180
QY 181 GTLCGYLAPELFVNVRKASTASQVTSFGILMAVAVLAGREVELPTEPLVTEAVCNQRNP 240
DB 181 gtligylapelvfvnvrkastasqvtsfgilmaavlagrevelpteplvteavcnqrnp 240
QY 241 SLALPAGETGEGIEIKELMOCSSSPKRPFOCLATKTPDEVQVFNEMNAAVST 300
DB 241 slalpagetgegietkelmocssspkrpfoclatktpdevqvfneemnaavst 300

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DB 241 slalpagnetgegietkelmqcwssephkdrpfqecldpctdevfqnemnaavst 300
QY 301 VDEFSQKSSNRNRSIPESGGCTEDGFRRTIENQHSRNDVWSEKLNLEPPSS 360
DB 301 vdfslqksnrfrfsipesggctedgfrtlenqhsrndvwmsewlnleppss 360
QY 361 VPKKPSLTKRSRAQEQVPOAWTACGSSDSMAOPQPFETSTFRNQPSTSGTSPG 420
DB 361 vpkcpstlkrssraqeqvpawtactgssdsmaqppqfettstfrnqpstsgtspg 420
QY 421 PRNGAGEROGMNSC 436
DB 421 prngagertgmwsc 436

```

RESULT 15
 AAB01529
 ID AAB01529 standard; Protein; 420 AA.
 AC AAB01529;
 XX
 XX 08-NOV-2000 (first entry)
 XX
 XX Kinase of death (KOD) delta death domain.
 DE
 XX KOD: kinase of death; programmed cell death; apoptosis; cancer;
 XX autoimmune disease; stroke; Alzheimer's disease; identification;
 XX kinase; ATP binding; death domain.
 XX
 XX Homo sapiens.
 OS
 XX US6096539-A.
 XX
 XX 01-AUG-2000.
 PD
 XX 10-JUN-1999; 99US-0329418.
 XX
 XX 10-JUN-1999; 99US-0329418.
 XX
 XX (ZENEC) ZENEC LTD.
 XX
 XX Gomes BC, Prosser JC, Kasof GW;
 XX
 XX WPI: 2000-523872/47.
 XX
 XX New nucleic acids encoding a protein activator of apoptosis for
 XX preventing, diagnosing and treating pathophysiological disorders
 XX related to apoptosis
 XX
 XX Claim 1: Columns 43-46; 32pp; English.
 XX
 XX The kinase of death (KOD) polypeptide is integral to the activation
 XX process of cellular apoptosis (programmed cell death). Apoptosis is
 XX needed to orchestrate biological maintenance of an organism during
 XX development as well as to preserve the normal function and fitness of
 XX tissues during a normal life span. Physiological conditions which
 XX result from aberrant apoptosis may be dire. Cancer and autoimmune
 XX disease may result when there is too little apoptosis as well as
 XX severe stroke damage or the neurodegeneration of Alzheimer's disease
 XX when there is too much apoptosis. The KOD polypeptide is useful for
 XX studying pathophysiological disorders related to apoptosis as well
 XX as for identifying compounds that modulate biological and/or
 XX pharmacological activity of the native mediator of apoptosis.
 XX In controlled tests, destruction of the kinase active, ATP binding
 XX site or removal of the whole kinase domain has no effect on the
 XX killing rate of KOD. However, loss of the death domain removes the
 XX killing activity of KOD.
 XX
 XX Sequence 420 AA;

Query Match 77.3%; Score 2145.5; DB 21; Length 420;
 Best Local Similarity 98.3%; Pred. No. 2.7e-159;

Matches 413: Conservative 1; Mismatches 5; Indels 1; Gaps 1:

```
OY 1 MSCVKKLMPGAPAPPLVSIIELENOELVGTGCGTYFPAQHRKNGIDVAVKIVMSKAISRE 60
    |||
Db 1 mscvkk1wpsqappp1vsiie1enqelvgkg9glvtrqhrkwygdvaavk1vnska1sre 60
    |||
OY 61 VKAMASIDNEFVLRLEGVIEKVN--DQDPKPALVTKFMENGSLGGLQSOCPAPMPILCR 119
    |||
Db 61 vkamaaidnefv1rllegviekvg9sqdpkpalvckfmenqslgllq9qcp1rmp1lcr 120
    |||
OY 120 LKEVYLGMFYLHDONPVLLHRDLKPSNVLPPELHVXKLADFGLSTRQSGSGSGTSGSEP 179
    |||
Db 121 lkevvylgmfy1hdqnpvll1hrdlkpsnvll1dpelhvkladfg1stfg99sgsgcgsgsep 180
    |||
OY 180 GGTUGYLAPELVNVRKASTASDVYSGIIMAVLAGREVELPTEPSLYTEAVCNQRNR 239
    |||
Db 181 ggt1gy1apellfvnvrka1s1advy1sg1lmwv1ag1revellpteps1ly1eavcnrqn1r 240
    |||
OY 240 PSLAELPQAGPETPGLEGKBLMQLCWSSEPKDRPSFQECLPKTDVFOYENNNNAAYS 299
    |||
Db 241 ps1aelpqagpetcpg1eg1kelmq1cwasepkdrps1fgeclp1ktdv1fgyenmmaavs 300
    |||
OY 300 TVRDFLSQLKSSNRRESTIPESGCGTEMDGFRRTIENQHSRNDVNVSENLKXNLDEPPS 359
    |||
Db 301 tvrdf1sq1ksnr1rfs1pesg9g3temdg1rr1lenqhsrndvnmvsewlnk1nlepp1s 360
    |||
OY 360 SVPRKCPSLTKRSRAQEDVYQAWTAGTSSDSMAQPPQTPETSTFRNQMPSTSTGTPSP 419
    |||
Db 361 svprkcp1sltk1raraqeedvypqaw1ag1tsd1smaqp1tpet1stfrnqmp1st1stg1tp1sp 420
    |||
```

Search completed: August 13, 2002, 22:07:31
Job time: 3313 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 21:16:13 : Search time 42.77 Seconds
(without alignment)
1166.013 Million cell updates/sec

Title: US-09-762-491-6

Perfect score: 2774

Sequence: 1 MSCVKLMPSGAPALYSIE.....PKDEANSRPGQWTHSGK 519

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : PIR_71:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445.5	16.1	656	2 I49299	receptor interacti
2	433	15.2	671	2 T09479	serine/threonine p
3	321.5	11.6	667	2 T47482	receptor-like prot
4	321	11.6	567	2 JCS957	transforming growt
5	321	11.6	606	2 JCS956	transforming growt
6	320.5	11.6	688	2 T48176	receptor like prot
7	318.5	11.5	579	2 JCS955	transforming growt
8	314.5	11.3	847	1 A53800	mixed-lineage prot
9	307	11.1	685	2 T48177	receptor like prot
10	307	11.1	1029	2 H86179	hypothetical prote
11	303	10.9	954	1 S68178	hypothetical prote
12	302	10.9	821	2 T48400	mixed-lineage prot
13	302	10.9	829	2 T07406	serine/threonine-p
14	299	10.8	848	2 H87950	probable protein k
15	299	10.8	855	2 T20082	protein f332.2 [1
16	298	10.7	613	2 T77483	hypothetical prote
17	298	10.7	900	2 T04839	receptor like prot
18	295.5	10.7	512	2 S21171	protein kinase hom
19	294.5	10.6	736	2 T05157	activin receptor s
20	292.5	10.5	963	2 T09911	protein kinase hom
21	290.5	10.5	513	1 JQ1486	probable kinase/th
22	290.5	10.5	513	1 A39896	activin receptor I
23	290.5	10.5	513	2 I45850	activin receptor I
24	290	10.5	655	2 H96692	activin receptor t
25	290	10.5	1171	2 T12956	probable receptor
26	289.5	10.4	513	2 A49193	hypothetical prote
27	289.5	10.4	513	2 S27258	type II activin re
28	289.5	10.4	513	2 D84525	activin receptor t
29	289.5	10.4	656	2 B86289	probable protein k
					probable serine/th

30	289	10.4	627	1 JCS534	protein kinase 1 (
31	288	10.4	396	2 H86301	hypothetical prote
32	287.5	10.4	394	2 J00229	mixed-lineage prot
33	287.5	10.4	516	2 A48678	activin receptor I
34	287.5	10.4	682	2 T48175	receptor like prot
35	287	10.3	553	2 T04683	hypothetical prote
36	286.5	10.3	514	2 J01317	activin receptor p
37	286	10.3	1248	2 B96827	hypothetical prote
38	285.5	10.3	513	2 S23089	activin receptor t
39	285.5	10.3	669	2 T08960	serine/threonine-s
40	285.5	10.3	984	2 A39753	protein-tyrosine k
41	284.5	10.3	849	1 T09349	S-receptor kinase
42	284	10.2	567	2 H84770	probable receptor-
43	284	10.2	975	2 I48974	receptor-protein t
44	283.5	10.2	355	2 G96813	hypothetical prote
45	283.5	10.2	406	2 T52626	probable mitogen-a

ALIGNMENTS

RESULT 1
149299
receptor interacting protein RIP - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1996 #sequence,revision 09-Mar-1996 #text_change 05-Nov-1999
C:Accession: I49299
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
Cell 81, 513-523, 1995
A:Title: RIP: a novel protein containing a death domain that interacts with Fas/ADO-1.
A:Reference number: A56913, MID:95377838
A:Accession: I49299
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-656 <RSS>
A:Cross-references: EMBL:U25995; NID:g829618; PID:AB60487.1; PID:g829619
A:Genetics:
A:Gene: RIP
A:Superfamily: protein kinase homology
F:15-293/Domain: protein kinase homology <Kin>

Query Match	16.1%	Score 445.5	DB 2	Length 656
Best Local Similarity	26.2%	Pred. No. 5.9e-14		
Matches 158	Conservative	89	Mismatches 205	Indels 151
			Gaps 23	
QY	15	LVYIEPLNDELIVGKDGPGVYRAOHRKRGVDVAKYIN-----SKATSRKYKAMASL 67		
DB	12	MASDLEKTDL-DGGGFKVSLCYHRSHGVILKVTGPNRAEYEVLEBGLAMRRL 70		
QY	68	DNEFVLRLEG-VIEKVNMDQPPALVTKEMENSLGGLAQSCPRPMLCRULKEVYL 126		
DB	71	RHSRVYLLDIIIEEGNY-----SLVMEYMEKMTLMVLTQDVLSLKGRHIVEALE 124		
QY	127	GMFLHDPNIVLHLRDLKPSNVLPPELHVKLADRGSLTFQSGSQ-----SGT 174		
DB	125	GMCLTHDKG--VTHDKLDPENITLDRPHIKRADGVASFTHNKLKREKDNOKNKSST 182		
QY	175	GSGEPTGTLGLAPLFLVAVNKRASDVYSFGTLMAYLAGAEVTLPEPRLVYEAAC 234		
DB	183	TRKNNGSTLYTMAPRHLINDIMAKPTEKSDVYSFGIVLWALPAKE---PRE-----NVIC 234		
QY	235	NRQ-----NRPSLAELPQAGPETPGLEGKELMQLQNSSEKDRPSF---QECLEK 282		
DB	235	TEQFVICIKSGNPNVPEILEYCPRE-----IISMERCHQAIPEDRPFLGLIEBFRFP 289		
QY	283	TDEVF-QVNNNNNAVSTVYKDFLSQLKSSNRPS-----IPES----- 320		
DB	290	YLSHFEEYVEDV---ASLAKETPQPSVLORMFSLOHDCVLPSPSNSNGORGLHSSO 346		
QY	331	--GGGTENDGFRRTTENDSHRDVAVSEMLNK-----LNL 354		
DB	347	GLONGPVEESWFSSEYSPEDENDRSVQAKLQEEASYHAGTFAEKTKRQPRONEAYNR 406		

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OY 355 EEPSSVPPKKGSLIKRBRAGEEVPQAMNAG-----SSDSMAQPPQPPPEST-FRQ 407
Db 407 EEEKRRRVSHIDPPAQQRAR---ENIKSAGARGSDSTTSKGIAYOLSPATQTVWNG 463
OY 408 MPSTSTGTPTSPGPGKNGCAEROGMNSCTPEPN-----PVTERPLVN-----IX 453
Db 464 LYNHGKGTGTGGVWYVPMNLSONYSTTKTPVPEPTNIPSTPTWYVYFSGPADDLIKYTF 523
OY 454 NCSGVQGDNNLTLMQQTTLPTMGLAPSGKGGLDHPPEVGSQSGREPDPEAMSPQGY 513
Db 524 NSSCIQIGNNHYMDV-----GLNSQPPNNYCK-----EESTSRHQALF 561
OY 514 NHS 516
Db 562 DNT 564

```

RESULT 2
T09479
sarine/chreonine protein kinase (EC 2.7.1.-) RIP - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C:Accession: T09479; 138992
R:Hung, J.; Hsu, H.; Balchwal, V.R.; Goeddel, D.V.
submitted to the EMBL Data Library, August 1998
A:Accession: T09479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-671 <HUG>
R:Stross-references: EMBL:U50062; NID:g3426026; PID:g3426027
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, B.; Seed, B.
Cell 81, 513-523, 1995
A:Title: RIP: a novel protein containing a death domain that interacts with Fas/Apo-1 (C
A:Accession number: A56913; MUID:95277698
A:Accession: 138992
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 300-513, 'S', 515-671 <RES>
A:Cross-references: EMBL:U03994; NID:g829616; PIDN:AAC50137.1; PID:g829617
C:Genetics:
A:Gene: RIP
A:Keywords: ARE binding; phosphotransferase

Query Match	15.28	Score 423	DB 2	Length 671
Best Local Similarity	25.38	Pred. No. 6.8e-13		
Matches 145	Conservative 95	Mismatches 186	Indels 146	Gaps 22

Qy	17	SIEELNDELGVKDGCFETVPAQHRMG-----YDAVAVIKVNSKAI\$REVKAMASLDN	69
Db	14	SSDPE\$E\$E\$L-D\$G\$G\$F\$V\$K\$C\$H\$R\$R\$O\$G\$M\$M\$K\$V\$K\$P\$C\$H\$E\$H\$E\$A\$K\$M\$M\$H\$R\$H	72
Qy	70	E\$V\$L\$R\$E\$A\$V\$E\$K\$Y\$M\$D\$D\$P\$R\$A\$V\$T\$F\$M\$E\$N\$G\$S\$A\$G\$S\$O\$C\$R\$P\$P\$C\$R\$C\$K\$T\$K\$V\$V\$G\$M\$F	129
Db	73	S\$R\$V\$K\$L\$G\$V\$-----I\$E\$G\$K\$Y\$S\$L\$M\$E\$Y\$M\$E\$K\$G\$N\$M\$H\$V\$K\$A\$E\$N\$S\$T\$P\$L\$S\$V\$G\$R\$I\$E\$I\$E\$G\$M\$C	127
Qy	130	Y\$H\$O\$Q\$N\$V\$V\$L\$H\$R\$D\$L\$K\$S\$N\$V\$L\$P\$D\$E\$L\$V\$K\$L\$D\$G\$L\$S\$T\$F\$O\$G\$G\$S\$O-----S\$G\$T\$G\$S\$G	177
Db	128	Y\$H\$O\$Q\$N\$-V\$H\$K\$D\$L\$K\$P\$N\$H\$L\$Y\$D\$N\$D\$F\$H\$K\$I\$A\$D\$G\$A\$S\$F\$K\$M\$S\$K\$L\$N\$E\$H\$N\$E\$L\$R\$E\$Y\$D\$G\$A\$K	184
Qy	178	E\$P\$G\$T\$G\$Y\$A\$P\$E\$H\$V\$N\$R\$R\$A\$S\$T\$A\$S\$V\$Y\$S\$G\$I\$M\$A\$V\$L\$A\$G\$R\$E\$V\$L\$P\$T\$E\$P\$S\$V\$Y\$E\$A\$V\$C\$N\$R\$O	237
Db	185	K\$N\$G\$T\$Y\$M\$A\$P\$E\$H\$D\$V\$N\$A\$R\$P\$T\$E\$K\$S\$D\$V\$T\$S\$F\$A\$V\$V\$M\$A\$F\$N\$K\$-----P\$Y\$R\$-----M\$A\$T\$E\$Q\$	236
Qy	238	-----N\$R\$P\$S\$L\$E\$L\$Q\$A\$G\$P\$E\$T\$P\$G\$L\$E\$G\$K\$L\$E\$L\$M\$O\$C\$M\$S\$E\$P\$D\$R\$S\$P\$E\$C\$L\$P\$K\$D\$E\$V\$O	288
Db	237	L\$M\$K\$G\$N\$R\$D\$V\$D\$D\$I\$E\$Y\$C\$P\$R\$-----I\$T\$S\$M\$K\$C\$M\$E\$N\$P\$E\$A\$R\$T\$F-----P\$G\$T\$E\$E\$N\$R\$P	287
Qy	289	-----M\$E\$N\$K\$M\$A\$A\$V\$Y\$K\$D\$F\$L\$S\$Q\$K\$S\$N\$R\$F-----S\$T\$P\$E\$S\$-----	330
Db	288	F\$Y\$S\$O\$L\$E\$S\$V\$E\$D\$V\$K\$S\$E\$M\$A\$V\$V\$R\$M\$O\$S\$L\$D\$C\$V\$A\$V\$S\$S\$N\$S\$N\$A\$T\$E\$D\$P\$G\$S\$L\$H\$S\$O	347

[illegible]

```

RESULT 3
747482
N:Alternat-like protein kinase - Arabidopsis thaliana
N:Alternate names: protein F18N1.180
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 (sequence_revision 20-Apr-2000 text_change 02-Sep-2000
C:Accession: T47482
R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Kewes, H.W.; Lemcke,
Submitted to the Protein Sequence Database, February 2000
A:Reference number: 324467
A:Accession: T47482
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-667 <ORF>
A:Cross-references: EMBL:AL132953
A:Experimental source: cultivar Columbia; BAC clone F18N1.1
C:Genetic:
A:Map position: 3
A:Note: F18N1.180
A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

```

[illegible]

RESULT 4
JC3937
transforming growth factor-beta activated kinase (EC 2.7.-.-) 1c - human
!Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Mar-2000
 C/Accession: J05957
 R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
 Biochem. Biophys. Res. Commun. 243, 545-549, 1998
 A>Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-ind
 A:Reference number: J05955; MUID:9815801
 A:Accession: J05957
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-367 <SAK>
 A:Cross-References: DBJ:AB009358
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: phosphotransferase

Query Match 11.6% Score 321; DB 2; Length 567;
 Best Local Similarity 26.6% Pred. No. 3.2e-08;
 Matches 134; Conservative 77; Mismatches 182; Indels 110; Gaps 26;

OY 11 APAPVSI-----ELENOELVKGDFGVFRADHRK--GYDAVATVNS-----KAISRE 60
 DB 21 APSOVLNFEIDYKEIEVEEVGKAGFVCKA---KWRKADVAIKQIESSEKRAFIYE 77
 OY 61 VKAMASIDNEFLRLGV-IEKVMNDODPKPALVTKEMENGLSGLIOSQCRP----- 113
 DB 78 LRQLSRVNHNPIVLYKACLNPIV-----CLVMEYAEGLSYNVLHGAEPPLPYTAH 129
 OY 114 ---WPLLCRLKLEEVLYGMYLHDNP-VLHRODKPSN-VLPPELVHVLADFG-----LS 164
 DB 130 AMSMCLQCS-----QGVATLHSMQPKALIRDLKPNLLVAGTVLACIDFGACDIO 183
 OY 165 TFOGSGSGTSGSEPGGTGLYAPLPELVNRRKASTADYVSGIIMAVLAGREV--EL 222
 DB 184 THMTNNK-----GSAMMAPEVFECSN--YSEKCDVFSMGIIMEVITRRKPFDEI 232
 OY 223 PTEPSLYEAVCNRRPSLAEI-POAGPETPGLGELKELQIOWMSSEPRDRSPDECT-- 280
 DB 233 GGPATFIMAVHNGTRPPLIKLPRP-----IESLMTKMSKDPQSRPSMEIYKI 283
 OY 281 -----PKTDEVFQMV-----ENNNAAVSTVKDFLSOLKSNRRFSIPSGGGGTEM 327
 DB 284 MTHLMRYFPQADEPLQYPCQYSDGQSHSAT--GSPNDIASTN-----TSNKSOTNM 335
 OY 328 DGFRRP-----IENQSHNDVMSSEMLKLEPPSSVPKRCP--SLTKRSRAQEOV 379
 DB 336 EQVPANNDITIKRLSKLKNQAKQOESGRSLGASGSEVESLPTSGCKRMSADNDEI 395
 OY 380 PQAWTACTSDSMAPQPTPTSTFRN--QMPSTSTGTSPSPRQNGAERQGMWMSCR 437
 DB 396 -EARIATTAISKPRKGR-KTASGNTLDVPELVISGNGPRRRSIDOLTVTG----- 447
 OY 438 TPEPNEVTGR--PLVNIYNCSG 457
 DB 448 -TEPGVSSRSSSPSVRMITTS 469

RESULT 5

transforming growth factor-beta activated kinase (EC 2.7.-.-) 1b - human
 C/Species: Homo sapiens (man)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C/Accession: J05956
 R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
 Biochem. Biophys. Res. Commun. 243, 545-549, 1998
 A>Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-ind
 A:Reference number: J05955; MUID:9815801
 A:Accession: J05956
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-606 <SAK>
 A:Cross-References: DBJ:AB009357; NID:G2924625; PIDN:BA02026.1; PID:G2924626
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: phosphotransferase

Query Match 11.6% Score 321; DB 2; Length 606;
 Best Local Similarity 26.6% Pred. No. 3.5e-08;
 Matches 134; Conservative 77; Mismatches 182; Indels 110; Gaps 26;

OY 11 APAPVSI-----ELENOELVKGDFGVFRADHRK--GYDAVATVNS-----KAISRE 60
 DB 21 APSOVLNFEIDYKEIEVEEVGKAGFVCKA---KWRKADVAIKQIESSEKRAFIYE 77
 OY 61 VKAMASIDNEFLRLGV-IEKVMNDODPKPALVTKEMENGLSGLIOSQCRP----- 113
 DB 78 LRQLSRVNHNPIVLYKACLNPIV-----CLVMEYAEGLSYNVLHGAEPPLPYTAH 129
 OY 114 ---WPLLCRLKLEEVLYGMYLHDNP-VLHRODKPSN-VLPPELVHVLADFG-----LS 164
 DB 130 AMSMCLQCS-----QGVATLHSMQPKALIRDLKPNLLVAGTVLACIDFGACDIO 183
 OY 165 TFOGSGSGTSGSEPGGTGLYAPLPELVNRRKASTADYVSGIIMAVLAGREV--EL 222
 DB 184 THMTNNK-----GSAMMAPEVFECSN--YSEKCDVFSMGIIMEVITRRKPFDEI 232
 OY 223 PTEPSLYEAVCNRRPSLAEI-POAGPETPGLGELKELQIOWMSSEPRDRSPDECT-- 280
 DB 233 GGPATFIMAVHNGTRPPLIKLPRP-----IESLMTKMSKDPQSRPSMEIYKI 283
 OY 281 -----PKTDEVFQMV-----ENNNAAVSTVKDFLSOLKSNRRFSIPSGGGGTEM 327
 DB 284 MTHLMRYFPQADEPLQYPCQYSDGQSHSAT--GSPNDIASTN-----TSNKSOTNM 335
 OY 328 DGFRRP-----IENQSHNDVMSSEMLKLEPPSSVPKRCP--SLTKRSRAQEOV 379
 DB 336 EQVPANNDITIKRLSKLKNQAKQOESGRSLGASGSEVESLPTSGCKRMSADNDEI 395
 OY 380 PQAWTACTSDSMAPQPTPTSTFRN--QMPSTSTGTSPSPRQNGAERQGMWMSCR 437
 DB 396 -EARIATTAISKPRKGR-KTASGNTLDVPELVISGNGPRRRSIDOLTVTG----- 447
 OY 438 TPEPNEVTGR--PLVNIYNCSG 457
 DB 448 -TEPGVSSRSSSPSVRMITTS 469

RESULT 6

receptor like protein kinase - Arabidopsis thaliana
 N/Alternate names: protein F7A7.70
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Sep-2000
 C/Accession: T48176
 R:Bevan, M.; Terry, N.; Ardiles, W.; Buysjaert, C.; Dasseville, R.; De Clerck, R.;
 ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: 224487
 A:Accession: T48176
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-688 <BEV>
 A:Cross-References: EMBL:AL161946
 A:Experimental source: cultivar Columbia; BAC clone F7A7
 C:Genetics:
 A:Map position: 5
 A>Note: F7A7.70
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 11.6% Score 320.5; DB 2; Length 688;

Best Local Similarity 31.4% Pred. No. 4.2e-08;
 Matches 101; Conservative 66; Mismatches 116; Indels 37; Gaps 15;

OY 22 ENOELVKGDFGVFRADHRKQID-VAVKTVNSKAISREVKAMASIDNEFLRLGLEGVIE 80
 DB 363 ENR-IVGTGDFGVFRGNLSSPSSDOIIVKKTIPNSQGVREPIAEISIGRLRRKRLVN 421

OY 81 KVMN-DQDQKPAVTKEMNGSLGLOSQCR-----PWPILCLRLKEVVLGMFLYLD 133
 DB 422 LOGCKCKMDLLIDYDIPKGLSLSLKSR-PROSGVAVLSMNRKFIAGISGLYLHHE 480
 OY 134 Q-NPVLLHRLKPSNVLDPELHVKLADFGLS-TFQCGSOSGTCGSEPGCTGLYLAPEL 191
 DB 481 EMEKVIYIHRDIPSNVLIEDDMNPRLGDFGLARLYERGOSQNT--TVVYGTIGYMAPEL- 537
 OY 192 VVNNRRASPDVYSGFGLMNAVLAGREVELPTEPSLYYA--VCNRQNRPSL--AEPLQ 247
 DB 538 -ARNKSSASGAFVAFVGLLEIYSGR---PTDSGTFIADVMELHARGEILNAVDR 593
 OY 248 APTPTGLEGLEKELM--OLCWSSEKDRPSQECLE-----PRTDEVQMVENNNNA 296
 DB 594 LDFGIDGVEARIALVAVGLLCHORPTSPSKIRLYRLNGLDDVDPEIDMWGSDSSMSD 653
 OY 297 AVSTVADFLSOLKSSNRPSIP 318
 DB 654 LGSNFGVYSDRASS---SVP 672

RESULT 7

JC5955

Transferring growth factor-beta activated kinase (EC 2.7.1.-) 1a - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Jul-1999 #sequence, revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: JC5955

R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
 Biochem. Biophys. Res. Commun. 243, 545-549, 1998

A:Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-Ind

A:Reference number: JC5955; MUID:98153801

A:Accession: JC5955

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-579 <SAR>

A:Cross-references: DDBJ:AB009356; NID:92924623; PIDN:BAA3025.1; PID:92924624

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C:Keywords: phosphotransferase

Query Match 11.58; Score 318.5; DB 2; Length 579;
 Best Local Similarity 25.78; Pred. No. 4, 3e-08;
 Matches 129; Conservative 74; Mismatches 165; Indels 133; Gaps 25;

OY 11 AAPLVSTF-----ELEQELVKGDCGTYVRAORRW-CYDAVATVNS---KAISRE 60
 DB 21 AFSQVLTNEEDIDYKEIEVEVVGARFVCKA---KMRKDAVAKQISESEKRAFTVE 77
 OY 61 VKAMASLDNEFLVRLGV-IEKVNMDQDPRPALVTKFMENGSLGLOSQCRP----- 113
 DB 78 LKRLSRVNHNPVIXLYGACLNPV-----CLVMEYASGSLYVNLHGAEPLPYTAH 129
 OY 114 ---WPLCLRLKEVVLGMFLYLDONP-VLLHRLKPSN-VLPDELHVKLADFG-----LS 164
 DB 130 AHSKLOQS-----QGVAVLHSMQKALIHRLKPNLLVAGGVLYLXICDFGACIOI 183
 OY 165 TFQCGSOSGTCGSEPGCTGLYLAPELFPVNNRASTASVYSFGILMAVLAGREV--EL 222
 DB 184 THTNTNKK-----GSAAMAAPEVSGSV--YSEKCDVFSGIIIMVYIRRRPFTEI 232
 OY 223 PREPSLYEAVCNRRNRSIAELPQAGPETPGLGLEKLEKLMWSEPPDRPSFOECL-- 280
 DB 233 GGPARRIMAVHNGTRPPLINKLP-----IESLMTKMSHSDPQRSMEIYKI 283
 OY 281 -----PKTDEVFOVY-----ENMNAAVSTVKDFLSOLKSSNRPSIPESGGGTEM 327
 DB 284 MTHLMKRPFGADEPLQYCOYSDGOSNSATST-----GSFIM 320
 OY 328 DGFRTTIENQSRNDVNVSEMLNKLNLSEPPSS--VPKPCSLTKRSRAQEQVQAWTA 385
 DB 321 D-----IASTNTSNK-----SOTNMEQVPATNDTIKRLSESLKLNQAKQSGSGLSL 368

OY 386 GTSSDSMAOP-POTPETSTFRNOMPS-----PTSTGPPSGPGNGCAEROGMNWSCRTP 439
 DB 369 GASRGSSVESLEPTSGKAMSDSEIARIAATNGCPRRRSIQDLTVTG-----T 421
 OY 440 EPNPVTGR---PLVNITYNCSG 457
 DB 422 EPGCVSSRSSSPSVRMITTSQ 442

RESULT 8

A53800

mixed-lineage protein kinase (EC 2.7.1.-) 3 - human

N:Alternate names: protein kinase PTK1; protein kinase SPRK

C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A53800; 158395

R:Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994

A:Title: Identification and characterization of SPRK, a novel src-homology 3 domain-c

A:Reference number: A53800; MUID:94253068

A:Accession: A53800

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-847 <GAL>

A:Cross-references: GB:U07747; NID:9464027; PIDN:AA19647.1; PID:9464028

R:Yang, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassar, N.D.
 Oncogene 9, 1745-1750, 1994

A:Title: MLK-3: Identification of a widely-expressed protein kinase bearing an SH3 do

A:Reference number: 158395; MUID:94239754

A:Accession: 158395

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-847 <RES>

A:Cross-references: GB:L32976; NID:9488295; PIDN:AAA59859.1; PID:9488296

C:Genetics:

A:Gene: GDB:MLK3; PTK1; SPRK

A:Cross-references: GDB:147955; OMIM:600050

A:Map position: 11q13.1-11q13.3

C:Superfamily: mixed-lineage protein kinase 3; protein kinase homology: SH3 homology

C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific prote

F:48-100/Domain: SH3 homology <SH3>

F:115-383/Domain: protein kinase homology <RTK>

F:123-131/Region: protein kinase ATP-binding motif

F:403-424/Region: leucine zipper motif

F:438-459/Region: leucine zipper motif

F:468-482/Region: basic

Query Match 11.34; Score 314.5; DB 1; Length 847;
 Best Local Similarity 21.58; Pred. No. 1e-07;
 Matches 157; Conservative 90; Mismatches 221; Indels 261; Gaps 29;

OY 4 VKLWPS-----GAPAP--LVSIELEQELVKGDCGTYVRAORRWKGYDAVAVI----- 51
 DB 92 VGIPTSNYSVRGGPPPCPVASFOELRLIEVYIGGFGYVGSNR--GELVAVAKAROD 149
 OY 52 -----VNSAISREYKAMASLDNEFLVRLGVIEKVNMDQDPRPALVTKFMENGSLG 105
 DB 150 PDEDISTASVYQOEARIFAMLAHPNIIALKACL-----EENLCLVMEYASGSLPSRA 204
 OY 106 LOSQCPPEPPLCLRLKEVVLGMFLYLDONPV-LLHRLKPSNVL-----PDELH--V 156
 DB 205 LAGRRPFP-VLYVNAVQIARGMHTLHCALVPIHRDLKSNHILLQPISSDDMBKTL 263
 OY 157 KLADFGLSTFGGSGSOSGTCGSEPGCTGLYLAPELFPVNNRAKST---ASDYISGILMA 213
 DB 264 KITDFGLAR-----EMKHTTQMSAAGTYAMNAPEVI-----KASTSKSDVMSFGVILME 314
 OY 214 VLAGREVELPTEP---SLVYEAVCNRRNRSIAELPQAGPETPGLGLEKLELMOLCNSSE 269
 DB 315 LITG---EYVYQIDCLAVAVGAVVNLTLF---IPSCPPP-----PAQIMADCAQD 362
 OY 270 PKDRPFP-----GQCLPKTD 284

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Db 363 PRRPFPASIILOALENAOVLREAPRDSFHSMOEGMKREIOGLFDELAKEREKILLSRE 297
QY 285 EVFQWVENNNMNA----- 297
Db 423 ELFRARAREQSQADLRREHLLAQMELEVERELTLLOQVDRERPHYRRRGTFKRSK 482
QY 298 -----VSTVKDFLSGL-----KSNRFSFSPSGOGGT----- 325
Db 483 LRAADGERISMEDPKRITVQASPGLDNRNRNVEFGPDSPFPFRALQLEPAERQO 542
QY 326 -----EMDGFRT-----IENQSHNDVASEM----- 348
Db 543 AMGRSPRLLEDSSNGERACWAMGSPSPKFGAQNRRSRDDEATVTLDSDDSPIGS 602
QY 349 -----LN-----KUNLEEPSSTPKR-----CPSTLRSAQEDQVPAWATGTSDD 390
Db 603 PSTPPALNGNPPRPSLEPEERKRPVPAERKSSSTGTPKILQIALLR-----GTALLSLGIG 658
QY 391 SMAQPPQTESTFRNQMSPTSTGTPRPGNQAERQGMMSCTPEPMPVTGRPLV 450
Db 659 RDQPPGCGP-----RERGESPTPTPTPAPCPTEPPSPPLICFSIKTDSPTPAPILL 714
QY 451 NIYNSGVGVGNNTLTMOOT-----TALPTMGLAPSGKR-GIQHPPVGSQSGPRDP 503
Db 715 DL-----GIYVQGRSAKSPRREERPGCVSPPTGTSARCTGTPRSPPLILSRPSP 770
QY 504 EAMSPQGV 512
Db 771 PLRSRIDPW 779

```

RESULT 9
T48177
receptor like protein kinase - Arabidopsis thaliana
N:Alternate names: protein F7A7 80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Sep-2000
C:Accession: T48177
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De
ewer, H.W.; Rudo, S.; Lemcke, K.; Meyer, K.F.X.
Submitted to the Protein Sequence Database, March 2000
A:Reference number: 224487
A:Accession: T48177
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-685 <BEV>
A:Cross-references: EMBL:AL161946
A:Experimental source: cultivar Columbia; BAC clone F7A7
C:Genetics:
A:Map position: 5
A:Note: F7A7 80
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc

Query Match 11.1%; Score 307; DB 2; Length 685;
Best Local Similarity 30.0%; Pred. No. 1.8e-07;
Matches 99; Conservative 64; Mismatches 115; Indels 52; Gaps 14;

```

QY 19 EELENDLVKDGKGFVPAQARKKGVAVAKYNSKAIS-----REYKAMASLDNERV 72
Db 355 EGKERNVVGTCGFCIVTGNIRSSDQIAVKITTPNSMGVREVAETESIGRLRHNL 414
QY 73 LRLEGVIERVNDODPKPALVTKFEMNGSLGLOSQCPK-----PAPFLCRLKEVVL 126
Db 415 VNIQGCGRHRN-----DLLLIYDIPNGSLDLSLYSK-PRRGAVALSMARFOIAKGAS 468
QY 127 GMEYTLIDQ-NPVLIRHDLKPSNVLPDELHYKLADFLS-TFGGSGSOSTGCGEGCGLG 184
Db 469 GLIYHBERDQIVYHRDVPNSVNLDSQNRDLDFALALYKSGOSCT--TVYVGIIG 526
QY 185 YLAPELFVAVNRKASVADSVSFGILMAVLAGREVELTPELVYEAQCNRMNPISAE 244

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Db 527 YMADELARNGN--SSASDVAFGVLLLEIVSGRK---PTDSGTFEIA-----DWNE 574
QY 245 LPQAPETPCL-----EGLKEIM---QLCMSSPKDRSFGQECPLP--KTDEVDM 289
Db 575 LQASGELSLAIDRLGSGVDEGEARLALAVGLCOHHKPRESRPLMYLVLYLRDEVDPE 634
QY 290 VENNMAAVSTVDFLSQK-----SSNRFS 316
Db 635 IHDNWGYSDSSKTDLSKLVGYISSDRASS 664

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RESULT 10
H86179
hypothetical protein [Imported] - Arabidopsis thaliana.
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H86179
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federjpiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Hughes, B.; Huizar, L.
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Morzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tello
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H86179
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1029 <STOD>
A:Cross-references: GB:AE005172; NID:G2494111; PIDN:AAB80620.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 11.1%; Score 307; DB 2; Length 1029;
Best Local Similarity 32.1%; Pred. No. 2.7e-07;
Matches 100; Conservative 49; Mismatches 103; Indels 60; Gaps 13;

```

QY 9 SGAPAPVSE-----ELENDLVKDGKGFVPAQARKK-CYDAVAKVNSK 55
Db 726 SFSEPAWVEIEAGITGQIITKMTLEDLHELGSQFGVY---YGNRGTDVAIKRINKS 782
QY 56 AIS-----REVAMASLDNERVLRLEGYERVNDODPKPALVTKFEMNGS 101
Db 783 CFSGGSSEQARQKTDKWRKARILANLHNRVAVATGYVPPD---GPGTMAVYTERVYNS 839
QY 102 LSGLDGSCPRPPLLCRLAKEVILGMEFLHNDQNPVLLHDLKPSNV---LPDELAV-K 157
Db 840 LRHVLQRK-DRRKKIMITY--DSARGMEYLIHKN--IVHDLKCDNLVNLADPQRIK 894
QY 158 LADGLSTFGGSGSGSGSGSGPGTGLYLAPELVNVRKASVADSVSFGILMAVLAG 217
Db 895 VGDGSLSRK--RNLVSGVGTGLPMWAPELLNGSSNRVSEKVDVSGIYMEILLG 951
QY 218 RE-----VELTRESLYEAVCRQNRPSLAELPQAGETGJLSKEIMDCSSSP 270
Db 952 EEPYANLHCVFEDDELGLSFGCIYVNNLTLPPEPCRA-----EMKRLKQCSFDP 1003
QY 271 KDRPSFOECLPK 282
Db 1004 GVRRSFEIYER 1015

```

RESULT 11
S68178
mixed-lineage protein kinase 2 (EC 2.7.1.-) - human
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
C:Accession: S68178; I38044; S32468
R:Dotov, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.R.; Sutherland, G.R.; Si

Bur. J. Biochem. 234, 492-500, 1995
 A>Title: Complete nucleotide sequence, expression, and chromosomal localization of human
 A:Reference number: 568178; MUID:96128179
 A:Accession: 568178
 A:Molecule type: mRNA
 A:Residues: 1-954 <DO>
 A:Cross-references: EMBL:X90846; NID:9971419; PIDN:CAA6351.1; PID:9971420
 R:Katoch, M.; Hirai, M.; Sugimura, T.; Teraoka, M.
 Oncogene 10, 1447-1451, 1995
 A>Title: Cloning and characterization of MST, a novel (putative) serine/threonine kinase
 A:Reference number: 138044; MUID:95249256
 A:Accession: 138044
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-461, 'A', 'V', '465-470', 'S', '477-806', 'R', '808-817', 'A', '819-954 <RES>
 A:Cross-references: EMBL:Z48615; NID:9758592; PIDN:CAA8531.1; PID:9758593
 R:Deroy, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
 Eur. J. Biochem. 213, 701-710, 1993
 A>Title: Identification of a new family of human epithelial protein kinases containing
 A:Reference number: S32467; MUID:93238756
 A:Accession: S32468
 A:Molecule type: mRNA
 A:Residues: 244-464, 'AQAAGKROPHOPALML' <DO>
 C:Genetics: GDB:MLK2; GDB:MST
 A:Gene: GDB:MLK2; GDB:MST
 A:Cross-references: GDB:362654; GDB:624810; OMIM:600137
 A:Map position: 19q13.1-19q13.2
 C:Superfamily: mixed-linage protein kinase 2; protein kinase homology; SH3 homology
 C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
 F:23-76/Domain: SH3 homology <SH3>
 F:96-364/Domain: protein kinase homology <KIN>
 F:104-113/Region: protein kinase ATP-binding motif
 F:384-405/Region: leucine zipper motif
 F:419-440/Region: leucine zipper motif
 F:449-463/Region: basic
 F:125,145,232,224/Active site: Lys, Glu, Asp, Lys status predicted

Query Match 10.9%; Score 303; DB 1; Length 954;
 Best local similarity 22.8%; Pred. No. 3.9e-07;
 Matches 150; Conservative 85; Mismatches 223; Indels 200; Gaps 32;

4 VILMP-----GAPRLVSI-----ELENOELVKGFGTVRAQHRKMGIDVAK 50
 DB 68 VQVPSNVYAPAPAPAGLDLQDRIPEHEQLDEEIIIGVGFGRVYALMR--GEVAVK 125
 OY 51 -----IYNSKAISREYKAAASLDNEFVRLKEGVIRKVMDDPKPALVTKFMENG 100
 DB 126 AARLDPEKDPATVTAQVQEARLFGALQHPRIIALRGACL-----NPHLCVNEVYARCG 180
 OY 101 SLGLTQSCPRPMPFLRLKLEVTYGMFYLDHONPV-LLRDLKPSN--VLDPDELH-- 155
 DB 181 ALSRYLAGRRVP-HVLYMNAVOYARGMNYLHNDAPPIIHRDLKSLINILILEALENNIL 239
 OY 156 -----VKLDFGLSTQSGSGSGSGGCGTGLYLADE-----LFPVNRKKA57ADVYS 206
 DB 240 ADTVLTLDFEGLAR---EMHKTTRKMSAAGYVMAEYVRLSLF-----SKSDVMS 288
 OY 207 FGILMAVLAG---REVELPTPEPLVYEAFCNRRNPRLAELPQAGPETPGLGLEKELM 262
 DB 289 FGVLLMELLTCEVYPREID---ALAVAYGVAMNKLTP---IPSCPRP-----FARLL 336
 OY 263 QLCNSPEKDRSPQECPLKTD-----EVQYENNNMAAVSTVYDEL-----S 306
 DB 337 EECMDPDRGRDPSILAKLEVTIDQSLRQMPLESHSHSLQEDMKLEIOMHDDTLTKRK 396
 OY 307 QKSSNRPSIPESGQGTEDKQGFRTIENSHNDVNSE---MINKLLEP----- 357
 DB 397 ELRSREELRLAAQQRQEQRLRRRDELAREMDIVRELLILMCSQSGKPRVRKK 456
 OY 358 -----PSSVPK-----CPSLTKRSRAQEDVQPMAGAGSSSM 392
 DB 457 GMPKRSRLKLKLDGSHSLSPSGFEHKITVQASPTLDKR-----GSDG- 500

OY 393 AQPOTPE-TSTFRNQMPSTSTGSPSPC-----PRGNO--CAEROCANMS 435
 DB 501 ASPSPSIIPRLAIRLRLTPVCCGSSSSSGSGTWSHGPPKKEELVGGKKKGRTW 560
 OY 436 -CRPPENPVTAARLVINICSGVQGDNNYLTWQOTLALPTGLAP----- 481
 DB 561 PSLQKEHYGGE-----RLKGLDEG-----SKWSSAPNLCGKSPKRTPIAPQFASLN 610
 OY 482 -----SGKRGQLQHP-----PVSGQSGPRDPKAW-----SRPGYVNRSGK 518
 DB 611 EMEPAEAEDGSGSVSPSPYSTPSTLSVLPALPSPGAPARAPRPPTSPAPRNHGARG 668

RESULT 12
 T84800
 serine/threonine-protein kinase ctrl - Arabidopsis thaliana
 N:Alternate names: protein F17C15.150
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_reviation 20-Apr-2000 #text_change 17-Nov-2000
 C:Accession: T84800; A45178
 R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, March 2000
 A:Reference number: 224492
 A:Accession: T84800
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-821 <BEV>
 A:Cross-references: EMBL:AL162506
 A:Experimental source: cultured Columbia; BAC clone F17C15
 R:Kieber, J.J.; Rothenberg, M.; Roman, G.; Feldmann, K.A.; Ecker, J.R.
 Cell 72, 427-441, 1993
 A>Title: CTRL, a negative regulator of the ethylene response pathway in Arabidopsis,
 A:Reference number: A45178; MUID:93161417
 A:Contents: Columbia
 A:Accession: A45178
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-468,470-821 <KIE>
 A:Note: sequence extracted from NCBI backbone (NCBI:124878)
 C:Genetics: GDB:150
 A:Map position: 5
 A:Introns: 216/31 317/2; 364/3; 399/2; 468/1; 560/1; 573/3; 596/3; 630/2; 658/3; 691/
 A:Note: F17C15.150
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP
 F:549-812/Domain: protein kinase homology <KIN>
 F:557-565/Region: protein kinase ATP-binding motif

Query Match 10.9%; Score 302; DB 2; Length 821;
 Best local similarity 33.6%; Pred. No. 3.7e-07;
 Matches 92; Conservative 44; Mismatches 96; Indels 42; Gaps 12;

20 ELENOELVKGFGTVRAQHRK--GIDVAVKYNK-----AISRYKAAASLDNE 70
 DB 550 DLNTERIGAGSGFYHRAE--HSGSDVAKILMEQDPHAERYEFLAEVAIMRLNHP 606
 OY 71 FVRLKEGVIRKVMDDPKPALVTKFMENGSLGLTQSCPRPMPFLRLK---EYVLG 127
 DB 607 NIVLFMGAV---QPPMLSTIVEYLSRGSLYRLHKSGARQDLERRRLSMAYDAKG 661
 OY 128 MFVLDHONPVTLHRDLKPSNVLPPBELHVKLADRGSLTQSGSGSGSGSGGCGTGLYLA 187
 DB 662 MNYLHNNRPPIVHRDLKSPNLLVDKRTVYKCDGSLRLK--ASTFLSKSAAGPEKMA 719
 OY 188 PELFVNNRKA57ADVYSFGILMAVLAGREVELPTPEPLVYEA---CNRRNPISLAE 244
 DB 720 PE--VLRDESNKSDVYSFGVYLMLATLQDPFGNLPAGVAVAVGFCR-----LE 771
 OY 245 LPO-AGPETPG-LEGLKELMDQCSSEPKDRPSF 276
 DB 772 IPRNLDPQVAALTEG-----CPTNEPKRPPSF 798


```

RESULT 13
707406
Probable protein kinase - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
C:Accession: T07406
R:Wang, Y.
submitted to the EMBL Data Library, May 1997
A:Reference number: E16016
A:Accession: T07406
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-829 <MAN>
A:Cross-references: EMBL:Y13273; NID:e1050452; PIDN:CAA73722.1; PID:e334294
A:Experimental source: strain UC828; sub-species M11
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold

Query Match 10.9%; Score 302; DB 2; Length 829;
Best Local Similarity 31.8%; Pred. NO: 3.7e-07;
Matches 102; Conservative 44; Mismatches 103; Indels 72; Gaps 15;

OY 25 ELVKGDFGYFRAQRHKV-GIVAVNKIV-----NSKAISEYKAMASLDNEVLAK 75
Db 559 EKIDAGSFYVHKRD--WHGSDVAVKILMEDFAERLKEFLREIVIMRLRPNIWV 615
OY 76 EGVIKYNMDDPRLALVTKFKENGSLGSLQSOCPR----PWPLRLRLKLVYLGFTL 131
Db 616 MGAIV-----TOPPLSLIVTEYLSRGSLSYRLHKPGAREVLDERRLC-MAYDVANGMNTL 669
OY 132 HDQNPVLLHRLRLKRSNVLPPDELHYKLADFGISTFGGS--QSGTGSGEQGTLYGLAPE 189
Db 670 HKRPPIYHKRDLSPRLIDYDKTKTYVICDFGSLSRKANTFLSSKTAAGTP-----ENWAP 725
OY 190 LFVAVNKRKASTADVSYSEGLIMAVLAGREVELPTPELSVYEA-VCKRQNRPSLAEL-PQ 247
Db 726 --VIRDEPSNKSVDVSYFVGLIMELATLQDPNNKINPQVLAAGFYRKRLDITPSDINPQ 783
OY 248 AGPPTGLEGLKMLQCMSEPKRDPQFQELPTPDEFOVVENNNMAAVTVKDFL-S 306
Db 784 -----VAIIIEACMANEPMKRPSF-----STIMDLAR 811
OY 307 OLKSNRRFSIPESGCGCTEM 327
Db 812 HLKS-----PLPPPHQIDM 825

RESULT 14
887950
protein F33E2.2 [Imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: B87950
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; NID:99369613; PMID:9831936
A:Note: see webstiles genome.wisc.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: B87950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-848 <SNOC>
A:Cross-references: GB:chr_I; PIDN:CA806544.1; PID:g3876653; GSEDB:GN00019; CESP:F33E2.2
C:Genetic:
A:Name: F33E2.2
A:Map position: 1

```

Query Match	10.88;	Score 299;	DB 2;	Length 848;
Best Local Similarity	27.08;	Pred. NO. 5.3e-07;		

[illegible]

OY 65 ASLDNEFVRLLEGVIEKVMMDOPKRALVTKFMENGSLGLOSOCPRPMLLCRLKEV 124
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 103 RHLEHQNIIEFVGYSK-----SPCYCIYMYCSKGGLCTVLSRMTITRELPAGQWKEI 157
OY 125 VLOMFYLRQNPVLRHRODKPSNVLPDEPLVXLADFGJSTFGGSGSGTSGCPGCTIG 184
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 158 ADGMHTLH-QNKV-IHRDLSFNILISAEDSIKICDPGSHMOKKMDSTWMSF--CGTYS 213
OY 185 YLAPELFVN--VNKRASSTADVYSFGILMAVLAGREVELP--TEPSLYEAVCNRONRP 240
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 214 KNAPEKIKKOPCNEKY---DYISRGVYLMMLT-RETPYANIAQNAIIFGVGTNLSLP 268
OY 241 SLAELPQAGPETPGLEGKELMQLCMSSEPRDRSPQECLEPKTD---EYFQVENNMNA 296
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 269 ---MPEBAP-----KGLVLTKOCLSOGRNRPFSHIRQHWELIFKPELFEETEEENOL 319
OY 297 AVSTVRDPLS--QLKSSNRR-----FSIPESGQGG-----TENDGFRTIENQSRN 341
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 320 AMDSYREFAKCIQYPTVTRDHCPSKSAFAMEEETQRRHREQLNHIKDIRNMYEMKLKRT 379
OY 342 DVA-----VSEMIKLNLEPPSSVPRKCPSLTKRSRAOEQVPOQAMT 384
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 380 NKHYDKLOCCFTELKKESELAEM--EKOLIERQONHONSPKAYAAPRAQLNGTPEBGY 437
OY 385 AGTSSDSMAQ-----PPOTPETSTFRNOMPSPTSTGTPSPGPRNGOAEROGNN 433
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
DB 438 DDMSSDEDVQPCRGSPYRCSTNTSSSSGVQSSPFSROSSRSASAGOOTRSEGAN 491

Search completed: August 13, 2002, 22:09:22
Job time: 3189 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compaq Inc.

OM protein - protein search, using sw model

Run on: August 13, 2002, 22:06:33 ; Search time 66.69 seconds

(without alignments)
1346.294 Million cell updates/sec

Title: US-09-762-491-6
Perfect score: 2774
Sequence: 1 MSCVKLMPSCAPPLVSTIELENOELVGKIDFGTFVRAQRKRGYAVATVNSKALISKE 519

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriophage:*
17: SP-archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2770	99.9	518	4 Q9Y572	Q9Y572 homo sapien
2	1389.5	50.1	486	1 Q9Q6L0	Q9Q6L0 mus musculu
3	1367	49.3	478	11 Q9Z2F5	Q9Z2F5 raltus norv
4	404.5	14.6	784	4 Q96T11	Q96T11 homo sapien
5	401.5	14.5	784	4 Q9H4D1	Q9H4D1 homo sapien
6	401.5	14.5	784	4 Q96KH0	Q96KH0 homo sapien
7	399	14.4	786	11 Q9ERK0	Q9ERK0 mus musculu
8	379	13.7	540	4 Q433J3	Q433J3 homo sapien
9	340	12.3	527	5 Q9B1Z5	Q9B1Z5 dictyostel
10	333	12.0	693	10 Q9SR87	Q9SR87 arabidopsis
11	324.5	11.7	564	4 Q9H1Y7	Q9H1Y7 homo sapien
12	320.5	11.6	667	10 Q9M0D7	Q9M0D7 arabidopsis
13	318.5	11.5	491	4 Q9KZ70	Q9KZ70 homo sapien
14	318.5	11.5	491	4 Q9KZ70	Q9KZ70 homo sapien
15	318.5	11.5	491	4 Q9KZ70	Q9KZ70 homo sapien
16	317.5	11.4	977	5 Q9VW24	Q9VW24 drosophila

17	317	11.4	606	11 Q923A8	Q923A8 mus musculu
18	314.5	11.3	847	4 Q16584	Q16584 homo sapien
19	313	11.3	1054	10 Q9FKL3	Q9FKL3 arabidopsis
20	312.5	11.3	616	13 Q73613	Q73613 xenopus lae
21	311	11.2	847	10 Q93XL9	Q93XL9 rosa hybrid
22	310	11.2	773	10 Q9C902	Q9C902 arabidopsis
23	310	11.2	850	11 Q9J315	Q9J315 mus musculu
24	308	11.1	1148	5 Q93VF6	Q93VF6 drosophila
25	308	11.1	1161	5 Q950N8	Q950N8 drosophila
26	307	11.1	685	10 Q9M019	Q9M019 arabidopsis
27	307	11.1	1029	10 Q23015	Q23015 arabidopsis
28	306	11.0	718	10 Q9LSR8	Q9LSR8 homo sapien
29	305.5	11.0	1066	4 Q9H2N5	Q9H2N5 homo sapien
30	304	11.0	806	10 Q9ZSD8	Q9ZSD8 lycopersico
31	304	11.0	829	10 Q9ZSD9	Q9ZSD9 lycopersico
32	303.5	10.9	608	10 Q9FPD4	Q9FPD4 arabidopsis
33	302	10.9	718	10 Q93ZK5	Q93ZK5 arabidopsis
34	302	10.9	829	10 Q24027	Q24027 lycopersico
35	301.5	10.9	763	10 Q9C903	Q9C903 arabidopsis
36	301.5	10.9	777	10 Q9C833	Q9C833 arabidopsis
37	299.5	10.8	1141	10 Q9LHP4	Q9LHP4 arabidopsis
38	299	10.8	855	5 Q01700	Q01700 caenorhabdi
39	298.5	10.8	478	4 Q9NTR4	Q9NTR4 homo sapien
40	298.5	10.8	566	4 Q9NTR2	Q9NTR2 homo sapien
41	298	10.7	613	10 Q9M1G4	Q9M1G4 arabidopsis
42	298	10.7	900	10 Q65474	Q65474 arabidopsis
43	296	10.7	451	4 Q9NTR3	Q9NTR3 homo sapien
44	296	10.7	539	4 Q9NTR1	Q9NTR1 homo sapien
45	295.5	10.7	512	13 Q9PSM0	Q9PSM0 xenopus lae

ALIGNMENTS

RESULT 1
ID Q9Y572 PRELIMINARY: PRT: 518 AA.
AC Q9Y572; 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RIP-LIKE KINASE.
GN RIP3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9927740; PubMed-10339433;
RA Yu P.W., Huang B.C., Shen M., Quest J., Chan E., Xu X., Nolan G.P.,
RA Payan D.G., Luo Y.,
RT "Identification of RIP3, a RIP-like kinase that activates apoptosis
RT and NF-kappaB".
RL Curr. Biol. 9:539-542(1999).
DR EMBL: A0156884; A0156885; A0156886; A0156887; A0156888; A0156889;
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Kinase; 1.
DR PRINTS: P00109; TYRKINASE.
KW PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 518 AA: 56901 MW: 38433CFFEBBD4151 CRC64;

Query Match 99.9%; Score 2770; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 5.3e-208;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCVKLMPSCAPPLVSTIELENOELVGKIDFGTFVRAQRKRGYAVATVNSKALISKE 60
DB 1 MSCVKLMPSCAPPLVSTIELENOELVGKIDFGTFVRAQRKRGYAVATVNSKALISKE 60

```

OY 61 VKAMASLDNEFLRLEGIEKVMNDODPKPALVTKFMENSGSLGSLQSCPPRPPPLCLR 120
DB 61 VKAMASLDNEFLRLEGIEKVMNDODPKPALVTKFMENSGSLGSLQSCPPRPPPLCLR 120
OY 121 LKEVYLGNFYLDONPVLLHRDLKPSNVLPDPELHVKLADFGSLSTFGGSGSGTSGSG 180
DB 121 LKEVYLGNFYLDONPVLLHRDLKPSNVLPDPELHVKLADFGSLSTFGGSGSGTSGSG 180
OY 181 GTLGLAELFVNVNRKASTASDVYSGIILMAVLAGREVELPTEPSLYEAVCRQRNP 240
DB 181 GTLGLAELFVNVNRKASTASDVYSGIILMAVLAGREVELPTEPSLYEAVCRQRNP 240
OY 241 STAEPLQAGPEPTGEGIKELMOLCNSSEPRDPSFQELPKTDEYFOVNNMNAAST 300
DB 241 STAEPLQAGPEPTGEGIKELMOLCNSSEPRDPSFQELPKTDEYFOVNNMNAAST 300
OY 301 VKDFLSQLKSSNRRESIPESGCGTEKDXGFRRTIENQHSNDVYSEWLKLNLEPPSS 360
DB 301 VKDFLSQLKSSNRRESIPESGCGTEKDXGFRRTIENQHSNDVYSEWLKLNLEPPSS 360
OY 361 VKKCPSLTKRSRAQEQVPOAMTACTSSDMAOPOTPTSTFRNMOMSPSTGSPSG 420
DB 361 VKKCPSLTKRSRAQEQVPOAMTACTSSDMAOPOTPTSTFRNMOMSPSTGSPSG 420
OY 421 PRNGNGARQGMNSCARTPEENPVYGRPLVNIYNGSGVQYGDNNYLTMOQTALPTMGLA 480
DB 421 PRNGNGARQGMNSCARTPEENPVYGRPLVNIYNGSGVQYGDNNYLTMOQTALPTMGLA 480
OY 481 PSNGRGLQHPFVPSOGCPKDPFVNSRPOGVNHSK 518
DB 481 PSNGRGLQHPFVPSOGCPKDPFVNSRPOGVNHSK 518

```

RESULT 2

```

OY 0902L0 PRELIMINARY; PRT; 486 AA.
AC 0902L0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RECEPTOR INTERACTING PROTEIN 3.
GN Rtp.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Pazdernik N.J., Donner D.B., Goebel M.G., Harrington M.A.;
RT "Mouse Interacting Protein 3 Does Not Contain a Caspase-Recruiting or
RT a Death Domain but Induces Apoptosis and Activates NF-kappaB.";
RT Mol. Cell. Biol. 19:0-0(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DB EMBL: AF178953; AAB03133.1;
DB InterPro: IPR000719; Euk_Pkinase.
DB InterPro: IPR002290; Ser_Thr_Pkinase.
DB InterPro: IPR001245; Tyr_Pkinase.
DB Pfam: PF00069; Pkinase.1.
DB PRINTS: PR00109; TYRKINASE.
DB PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DB PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KV ATP-binding; Serine/threonine-protein kinase; Transferase.
SO SEQUENCE 486 AA; 53336 MW; DD264E69187D3436 CRC64;

```

Query Match 50.18; Score 1388.5; DB 11; Length 486;
 Best Local Similarity 59.48; Pred. No. 3.6e-100;
 Matches 295; Conservative 49; Mismatches 130; Indels 23; Gaps 7;

```

OY 1 MSCVILMPSGAPA-PLVSIIELENGELVKGEGTVFRAQHRKMGDVAVKIVNSKAISR 59
DB 1 MSCVILMPSGAPA-PLVSIIELENGELVKGEGTVFRAQHRKMGDVAVKIVNSKAISR 59

```

```

OY 60 EVKAMASLDNEFLRLEGIEKVMNDODPKPALVTKFMENSGSLGSLQSCPPRPPPLCLR 119
DB 61 EVKAMASLDNEFLRLEGIEKVMNDODPKPALVTKFMENSGSLGSLQSCPPRPPPLCLR 120
OY 120 LKEVYLGNFYLDONPVLLHRDLKPSNVLPDPELHVKLADFGSLSTFGGSGSGTSGSG 177
DB 121 LKEVYLGNFYLDONPVLLHRDLKPSNVLPDPELHVKLADFGSLSTFGGSGSGTSGSG 180
OY 178 --EPGGLGLAELFVNVNRKASTASDVYSGIILMAVLAGREVELPTEPSLYEAVCN 235
DB 181 SRSQGGTIALVDPPELLFVNVNLKASKASDVYSGIILMAVLAGREVELPTEPSLYEAVCN 240
OY 235 RQRPSLAEPLQAGPEPTGEGIKELMOLCNSSEPRDPSFQELPKTDEYFOVNNMNA 295
DB 241 RQRPSLAEPLQAGPEPTGEGIKELMOLCNSSEPRDPSFQELPKTDEYFOVNNMNA 300
OY 296 AAVSTVDELSQLKSSNRRESIPESGCGTEKDXGFRRTIENQHSNDVYSEWLKLNLE 355
DB 301 AAVSEVHYLSQHRSSGRNLSRPSQGRTEKDCPRET-----MVSRLMDRLHLE 350
OY 356 EPPSSVPRKCPSLTKRSRAQEQVPOAMTACTSSDMAOPOTPTSTFRNMOMSPSTG 415
DB 351 EPPSGVPRKCP-----EPOADTSVGPATPAPTSDBVACTPQIPHTLPFGTTGVPVTE 406
OY 416 TPSPGRNGOGAARQGMNSCARTPEENPVYGRPLVNIYNGSGVQYGDNNYLTMOQTAL 474
DB 407 TPSPGRNGOGAARQGMNSCARTPEENPVYGRPLVNIYNGSGVQYGDNNYLTMOQTAL 465
OY 475 PT--WGLAPSGCRGLQ 489
DB 466 SSAKYDQADQPGRCRQ 482

```

RESULT 3

```

OY 0942P5 PRELIMINARY; PRT; 478 AA.
AC 0942P5;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HOMOCYSTEINE RESPONDENT PROTEIN HCRP2.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STEIN-WEISSER KYOTO;
RA Chen K.H., Tang J.;
RT "A homocysteine-respondent gene cloned from WKY VMSCs by differential
RT display";
RT Submitted (MAY-2001) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DB EMBL: AF036537; AAD02059.2;
DB InterPro: IPR000719; Euk_Pkinase.
DB InterPro: IPR002290; Ser_Thr_Pkinase.
DB InterPro: IPR001245; Tyr_Pkinase.
DB Pfam: PF00069; Pkinase.1.
DB PRINTS: PR00109; TYRKINASE.
DB SMART: SM00220; S_TKc.1.
DB SMART: SM00219; TYRKc.1.
DB PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DB PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KV ATP-binding; Serine/threonine-protein kinase; Transferase.
SO SEQUENCE 478 AA; 52234 MW; ED6C280C354E1977 CRC64;

```

Query Match 49.38; Score 1367; DB 11; Length 478;
 Best Local Similarity 59.68; Pred. No. 1.7e-98;
 Matches 292; Conservative 47; Mismatches 135; Indels 16; Gaps 6;

```

OY 1 MSCVKLMPGABA-PLVSIIELENOELVGKDGEGTFRAGRRMGVDAVAKIVNSKAISR 59
DB 1 MSSVKTMLAGASSISLYGSEEELENGEFGKGGFAGVARRHTAMNDVAVAKIVNSKISR 60
OY 60 EVKAMASLIDNEFVLRLEGVIERVNMDDOPKPAVLTKEFMENGSLSGLQSCRPMPILCR 119
DB 61 EVKAMNLKHEVNLILLSTENTLENDYVYGFALVTGMENGSLSGLQSCRPMPILCR 120
OY 120 LKEVVLGHPYLRHLDQNPVLLHDLKPSNVLPDPELVKADFLSTFGGSGSGTSG-- 177
DB 121 LLEEVVLGHCYLSLPSLPHDLKPSNVLLDPLKADFLSTFGGSGSGSGSGSR 180
OY 178 EPGGTGLYLAPELVNVRKASTADVYSPGILMNAVLAGREVELPTEPSLYEAVCNRQ 237
DB 181 DSGTGLAYLAPELLON-DGKASKADVYSPGVLTWVLAGEADEVDTKSLRGAVCNRQ 239
OY 238 NRPSLAELOAGPEPFGLEGLKELMQLCWSSEPKDRSPQECJPKTDEYFOVVENNMA 297
DB 240 RRPPLLELPDPDEPTEGLEGLELMTKCHMSEPKDRSPQECSTKNVYILVQKVDMA 299
OY 298 VSTVKKDFLSQLKSSNRFSIPSGGGTEMDGFRRTIENHSDVAVSEMLNKINLEEP 357
DB 300 VSKVKYLLSOYRSQDKLSARRSSCKGTEVDCPRETI-----VYEMLDRLHLEEP 349
OY 358 PSSVPRKCSLITRSRAQBEQVPOAWTAGTSSDSMAOPPGTPTSTFRNOMSPSTGTP 417
DB 350 SGSVPELISLTER-RGRASRCHATPACTSSDTLACTPQIPHTLPSRGTTPRAPFTETP 408
OY 418 SPGRNOCAGENQGMNSRTERPEPVYGRVLVNYICSGVQVGNNTLTMOQTALTPW 477
DB 409 GPDRKNGGGRNSNFWTWN-APNPMTGLQSLVLMNCSEVQIGQHNCSVQPRTAPEPK 467
OY 478 GLAPSGKRG 487
DB 468 EPAQFGRNG 477

RESULT 4
O96711 PRELIMINARY; PRT: 784 AA.
AC O96711;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE CDNA FLJ14518 FIS, CLONE NT2RM1000850, WEAKLY SIMILAR TO ANKYRIN R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isoqel T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nagatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamanoto J., Wakamatsu A., Nakamura Y., Nagelharl K., Masuko Y.,
RA Minomiya K., Iwayanagi T.;
RT "genomic cDNA sequencing project.";
RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK027424; BAB5102.1; -.
SQ SEQUENCE 784 AA; 86348 MW; 05B193EB4EB9E5AF CRC64;

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Query Match 14.6%; Score 404.5; DB 4; Length 784;
 Best Local Similarity 30.0%; Pred. No. 4,9e-23;
 Matches 128; Conservative 71; Mismatches 165; Indels 63; Gaps 16;

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OY 10 GARPPLVSTF-----ELENOELVGKDGEGTFRAGRRMGVDAVAKIVNSKAISR----- 58
DB 6 GTPMALALLTPTDAGEFTGEMRVGSGFGQYKVRHVMKMTWLALICSPSLHVDORERKE 65

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OY 59 --REKAMASLIDNEFVLRLEGVIERVNMDDOPKPAVLTKEFMENGSLSGLQSCRPMPIL 116
DB 66 LLEBAKMEKAPFRYILPYAGICR-----PVLGWEYMETGSLKELASE-PLPMDL 117
OY 117 LCRLKLVNGLFVLRHLDQNPVLLHDLKPSNVLPDPELVKADFLSTFGGSGSGTSG 176
DB 118 RFRILHETAVGNHFLCMAPPLHLDKPAHILDAHYHKKIDSPGLKANGSHSHDS 177
OY 177 GEP-GGTGLYLAPELVNVRKASTADVYSPGILMNAVLAGREVELPTEPSLYEAV-C 234
DB 178 MDGFEIATLPERLREKSRSLDTRKHVYSFAIVMGVLTOK-PPADCKNLHITMNV 236
OY 235 NRQRPLELAELOAGPEPFGLEGLKELMQLCWSSEPKDRSPQECJPKTDEYFOVVENNMA 294
DB 237 VKGRPELPVPCARPR--ACSHLIRLMQRCMOGDPVRVPTFOETSETEDLCEKPDDEV 294
OY 295 NAA-----VSTVKKDFLSQLKSSNRFSIPSGGGTEMDGFRRTIENHSDVAVSEMLNKINLEEP 348
DB 295 KETHADLDVSPPEPSEVVPARLRASAP-----TPNDYS-----LSL 335
OY 349 LNKLN-----LEPP-----SSVPRKCSLITRSR-AQBEQVPOAWTA-GTSSDSMAOP 396
DB 336 LQSIDSGVSOAVGPELRSSESKLPSSGCRRLGSSVDSAFSSRGLSLSTFEREP 395
OY 397 QTPETST 403
DB 396 STSDLGT 402

```

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RESULT 5
O9H4D1 PRELIMINARY; PRT: 784 AA.
AC O9H4D1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE DE PROTEIN KINASE.
GN DTK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-70549657; PubMed-10948194;
RA Baehr C., Rohrer A., Stempka L., Rincke G., Marks F., Gschwendt M.;
RT "DK, a novel protein kinase that interacts with protein kinase
RT Cdelta. Cloning, characterization, and gene analysis.";
RU J. Biol. Chem. 275:36350-36357(2000).
DR EMBL: AJ278016; CAC04247.1; -.
DR HSSP; P25963; IINK.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002390; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00023; ank. 10.
DR Pfam: PF00069; pkinase. 1.
DR PRINTS: PR01415; ANKYRIN.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00248; ANK. 10.
DR SMART: SM00221; STYKc. 1.
DR SMART: SM00220; S_TKc. 1.
DR SMART: SM00219; TYRKc. 1.
DR PROSITE: PSS0088; ANK_REPEAT. 9.
DR PROSITE: PSS0297; ANK_REPEAT_REGION. 1.
DR PROSITE: PSS0017; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PSS0013; PROTEIN_KINASE_DOM. 1.
RW ANK repeat, ATP-binding; kinase; Repeat; transferase.
SQ SEQUENCE 784 AA; 86407 MW; F3C7BD52A35A9F1 CRC64;

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Query Match 14.5%; Score 401.5; DB 4; Length 784;

Best Local Similarity 30.0%; Pred. NO. 8.3e-23;
Matches 128; Conservative 70; Mismatches 166; Indels 63; Gaps 16

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OY 10 GAPPALYSIE-----ELENOELVGKDGFGTVPRAOHNRMGIDVAKIVNSKAIS----- 58
Db 6 GTPVALALMTPTPAGEFTGMEKVGSGGGQYKKV/RHMKMTALIAICSPSLHYDDRENE 65
OY 59 --REVMAALDNEFVLRLEGVTEKVENNDOPKALTYTKNENGSTSLGQSCRRPPL 116
Db 66 LIEAKNRMBKAKRTTILYPAVYICRE-----PVLMEHETGSEKRLKASE-PLPMDL 117
OY 117 LCRLKEVYLGMFVLRHDQNPVLIHLDLAPSNVLPDPPELHYKLADFGLSTFGGSGSGTGS 178
Db 118 RFRRIHTAAGMNFELHGMCPPLHLHLDLPAHLIDALAHVHKIDFGLACNLSHSNOLS 177
OY 177 GEP-GGTGLGALBELVFNANRRASTASVVSFGILMAVYLAGREVELPTPEPLVEAV-C 234
Db 178 MDGLGFTGIATVLPERRIREKSRLEFDTRKHVSEFALVINGYLTQKK-PRADEKMTILINIKV 233
OY 235 NROHREPLALPQAGFETGGLGKELMQLGKNSSEPRDRSPDECPKTXIDVFQVENVNM 294
Db 237 VGRHREPLPVCAGARR--ACSHLLRLMOKMCGDPPVARTPELTISEEDCKECPDDEV 294
OY 295 NAA-----VSVADELISQLKSSN-RRFSIPESGGGTMDGFRRIENHSHNDVNSM 348
Db 295 KETAHLDLVSPPESEVYPARLRAASAP-----TNDNYS-----LSBL 335
OY 349 LNRKLN-----LDRPP-----SAPPKCKSLTKRRSR-AOEQVPAQWTA-GTSDSMADPP 396
Db 336 LSGLDSEVSGAVGPELRLSSSSSKRLSSSGKRLSGVSYDSASNSKGLSLSEFENP 397
OY 397 OTPEITS 403
Db 396 STSDLCT 402

RESULT 6
O96KRHO PRELIMINARY: PRT: 784 AA.
AC O96KRHO;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROBABLE DUAL-SPECIFICITY SER/THR/TYR KINASE.
GN ANKRD3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_Taxid:9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=FETAL KIDNEY AND FETAL LUNG;
RA Shimizu N., Kudoh J., Shibuya K.;
RT "Homo sapiens mRNA for ANKRD3, complete cds."
DR Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB047783; BAB56136.1; -.
KM KINASE.
SQ SEQUENCE 784 AA: 86408 MW: 7587DBD52A35A191 CRC64;
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Query Match	14.5%	Score 401.5	DB 4	Length 784
Best Local Similarity	30.0%	Pred. No. 8	3e-23	
Matches 128	Conservative 70	Mismatches 166	Indels 63	Gaps 16

Oy	10	GAPPLVSI-----ELENELVGNKGGCTPYRAHRKMGCDVAKVYNKSAIS-----	58
Db	6	CTPALALLLTPDAGETGCKHAKVSGSGFQVAKVKNVAKTKTKLAKCPSRLHYDNDREHRE	65
Oy	59	--REVKMAASLIDNEFVRLDEGVLEKYVMNDQKRALVTKFENGSGLSGLAQSCPRPML	116
Db	66	LLEAKKCHNAKFRYITLIPYVIGCR-----PVLGVMEYKETSSTLEKLLASR-PLPMDI	117
Oy	117	LCRLLEKVLVGMFYLHQDNPVLLHRLDKESNVLPDELHVKLADFGSLTGQGSQSCTGS	176

Db	118	RRRIIEHVAAGMNFILQMAPLLHDLAPAILLDIAHYVHKISDFCLAKNCGLSHSDLS	177
QY	177	GGP-GGTLGLTATLELVVNNRRKASADSVYFGLIMAVLAGHEVLPTEPSLYEAV-C	234
Db	178	MDGLRGTLALPERLRKRSRLPTDKKVVISFALVINGVLTKK-PFADKKIYILINVKY	236
QY	235	NKQNPISLAEIPAAGETPGLEGLKEIMQLCWSSEPPKDRPSPQECPLPTDEVFQVENVN	294
Db	237	VGHRRPELPVCARARR--ACSHLIRLMQRCMOGDPVRRPTQETISFTEDELCERPDDEV	294
QY	295	NNA-----VSYVDEFLSQLKSSN-RRFSIPESGGGTENDGFFARTIENQSRNDVYSEN	348
Db	295	KETADHDVMSPEPPSEVVPARLKASAP-----TFDNDYS-----LSEL	335
QY	349	LWKIK-----LEPP-----SSVPKCKSLTKRSR-AQEDQVQMAVTA-CRSSPMQNP	336
Db	336	LSQLDQGVCAVQEPPELRSSESKLPSSCGNRKLSGVASVDSAFSSKGLSLSFPERP	335
QY	397	QTEPTST 403	
Db	396	STSDLGT 402	
RESULT	7		
QSERKO			
ID	09ERK0	PRELIMINARY:	PRT: 786 AA.
DT	01-MAR-2001	(TREMblrel. 16, Created)	
DT	01-MAR-2001	(TREMblrel. 16, Last sequence update)	
DT	01-DEC-2001	(TREMblrel. 19, Last annotation update)	
GN	PKC-REGULATED KINASE PKA.		
GN	ANKMD3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI	taxid:10090;		
LN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C;		
RC	MEDLINE-12931027; PubMed-11278382;		
RA	Chen L, Halder K., Ponda M., Carlappa A., Rovitch D., Piliat S.;		
RT	"Protein Kinase C-associated kinase (PKC), a Novel Membrane-		
RT	associated, Ankyrin Repeat-containing Protein Kinase.";		
RL	J. Biol. Chem. 276:21737-21744(2001).		
DR	EMBL, AF302127; MAG50871.1; --		
DR	HSSP: P25963; 1IKN.		
DR	MGD: MGI:1919638; Ankrtd3.		
DR	InterPro: IPR002110; Euk_pkinase.		
DR	InterPro: IPR000719; Euk_pkinase.		
DR	InterPro: IPR004040; Ser_thr_kinase.		
DR	InterPro: IPR001245; Tyr_kinase.		
DR	Pfam: PF00069; pkinase; 1.		
DR	PRINTS: PRO1415; ANKYRIN.		
DR	PRINTS: PRO0109; TYRKINASE.		
DR	SMART: SM00248; ANK: 10.		
DR	SMART: SM00321; SYTKC: 1.		
DR	SMART: SM00320; SYTKC: 1.		
DR	SMART: SM00219; TYRKC: 1.		
DR	SMART: PS50288; ANK_REPEAT: 9.		
DR	PROSITE: PS50297; ANK_REPEAT_REGION: 1.		
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP: 1.		
DR	PROSITE: PS00011; PROTEIN_KINASE_DOM: 1.		
KW	ANK repeat; ATP-binding; Kinase; Repeat; Transferase.		
SO	SEQUENCE 786 AA; 86702 MW; 8DB98977F5004787 CRC64;		

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QY 20 ELENELVGTGDFGVFAQRKNGYDVAATYNSKAIS-----REVKAASLDNEF 71
DB 21 EFAGMEKVGSGGFGVYVVRVHVKMTLAKCSPSLVVDREMRMELLEAKKMEKAKRY 80
QY 72 VIALSEVIEKVMDDPKPALVTKFMNGSLGSLGLOSCPRPPLICRLKLEVLGMYL 131
DB 81 ILPVYRIC-----QEP-VGLVMEWMEGSLKELASE-PLPMDLFRIVHETVANGMFL 132
QY 132 HDONPVLRLDLPKSNVLPDELHVKLADGLSTFGGSGSGSGSEP-GGLGLYLAEL 190
DB 133 HCSAPPLLDLPANILDLADHYKISDFGLACNKGSHSODLSGLGLETIATLPPER 192
QY 191 FVANNKASTADYVSFGILMMAVIAGREVELPTPESLYEAVCNQNPRLAEPLQAPG 250
DB 193 IREKSLFETKIDVYSFAIVGWYVLTOKKPEADEKNTLHIMMYVKGHPDEL--PICRP 250
QY 251 EFTGLGLKELMQLCWSSEPKDRSPFQCLPKTDEYQVWENNMAAVSTVDFLSOLKS 310
DB 251 RPRACASLIGLMQRCHMDPQVRPTFQETISRETDLCERKDE-----VQDLAHE--- 300
QY 311 SNRRFSIPESGGGTEDMGFRRTIENQSHNDVWSEMTKLN-----LEPP-----SS 360
DB 301 PGKSSLSKSSARPSSRLKASAPPD-NDCSLSELSQLDSCISQTLGEPPELSRSS 359
QY 361 VPKKPSLTKRRSAQEQVQAWTACTSSDSMAOPQTPETSPFRNQNPSTGTSPSP 419
DB 360 SECKLPSGSSGKR-----LSGVSYDAFSSSGSLSTLSPERE---ASTDGLCP 404

RESULT 8
ID 043353 PRELIMINARY; PRT; 540 AA.
AC 043353;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SERINE/THREONINE KINASE RICK (RECEPTOR-INTERACTING SERINE-THREONINE KINASE 2).
GN RICK OR R1P2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98241596; PubMed=9575181;
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
RT "Rick, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates G95-mediated apoptosis.";
RT J. Biol. Chem. 273:12396-12300(1998).
RN 12
RP SEQUENCE FROM N.A.
RX Ozerksy P., Holmes A., Broly M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE=98307936; PubMed=9642260;
RA McCarthy J.V., Ni J., Dixit V.M.;
RT "R1p2 is a novel NF-kappaB-activating and cell death-inducing
RT kinase.";
RT J. Biol. Chem. 273:16968-16975(1998).
RN 14
RP SEQUENCE FROM N.A.
RX Thome M., Hofmann K., Burns K., Martillon F., Bodmer J.-L.,
RA Maltmann C., Tschopp J.;
RT "Identification of CARDIAC, a RIP-like kinase that associates with
RT caspase-1.";
RT Curr. Biol. 8:0-0(1998).
RN 15
RP SEQUENCE FROM N.A.
RA Slater M., Varon R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN 16

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RP SEQUENCE FROM N.A.
RC TISSUE=SKIN, AND MELANOMA;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF027705; AAC34970.1; -
DR EMBL: AC004003; AAC24561.1; -
DR EMBL: AF028530; AAC27222.1; -
DR EMBL: AF064824; AAC25668.1; -
DR EMBL: AF117829; AAC04634.1; -
DR EMBL: BC004553; AAC04553.1; -
DR Interpro: IPR001315; CARD.
DR Interpro: IPR000719; Euk_pkinase.
DR Interpro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF006619; Kinase; 1.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00221; STRC; 1.
DR PROSITE: PS02020; CARD; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KV ATP-binding, Kinase; Serine/threonine-protein kinase; Transferrase.
SQ SEQUENCE 540 AA; 61194 MW; 575A692239505792 CRC64;

Query Match 13.7%; Score 379; DB 4; Length 540;
Best Local Similarity 31.7%; Freq. No. 2,8e-21;
Matches 101; Conservative 62; Mismatches 126; Indels 30; Gaps 11;

QY 14 PLVSEIELENQELVGDGFGVFAQRKNGYDVAATYNSKAISREVKAAM 64
DB 11 PTIPYHKLADLRITLSGASGTVSARHADNRVQVAKHLIHPLDSEKDLREAEIL 70
QY 65 ASDNEVRLLEGVEIKVMDDPKPALVTKFMNGSLGSLGLOSCPRP---WPLLCRL 121
DB 71 HKAFESIILPILGICNEPPEF-----LGIVTEYMPGSLNELKRTKTEYDVAWPLARFRL 125
QY 122 KEVYLFYLDONPVLLRLDLPKSNVLPDELHVKLADGLSTFGQ-GGSGSGSGSEP 179
DB 126 HEIADGVNVLHNNTPLEPLHDLKQNLILDNHFFVKIADGLSKRMKMSLSQSRSSKAP 185
QY 180 -GGTIGYLAPELF-VVNNKASTADYVSFGILMMAVIAGRE-VELPTPESLYEAVCNR 236
DB 186 EGGTIYMPENEPQKSRASIKKHDIYSAVITWEVLSKQPFEDVTNPDIQIMYSV-SQ 244
QY 237 QNRSLAE--LPQAGETGLEGLELMQLCWSSEPKDRSPFQCLPKTDEYQVW--N 292
DB 245 GHRVYNESLPT--DIPHRARMTSLIESGMAQNPDRSPFLKLELPVLRFEET 301
QY 293 NMNAAVSTVDFLSOLKSS 311
DB 302 FLEAVIOIKTKTLOSVSSA 320

RESULT 9
ID 09B125 PRELIMINARY; PRT; 527 AA.
AC 09B125;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SHK1 PROTEIN.
GN SHK1.
OS Dictyostellium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellidae; Dictyostellium.
OX NCBI_TaxID=44689;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=21172738; PubMed=11274054;
RA Montaliis J.;
RT "An SH2-domain containing kinase is a negative regulator of the
RT phosphatidylinositol-3 kinase pathway.";

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RL Genes Dev. 15:687-698(2001).
 CC -1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AJ297966; CAC35360.1.
 DR HSSP: P08611; IAD5.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR000980; SH.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00252; SH2.1.
 DR SMART: SM00220; S_TKc.1.
 DR SMART: SM00219; Tyrc.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50001; SH2.1.
 DR ATP-binding: Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 527 AA; 59505 MW; 19876B03B78F98E CRC64;

Query Match 12.3%; Score 340; DB 5; Length 527;
 Best Local Similarity 26.5%; Pred. No. 3e-18;
 Matches 128; Conservative 69; Mismatches 154; Indels 98; Gaps 23;

QY 14 PLVSIELNDELNGKDGCGTFRPAQHRKRGYDVAVKI-----VNSKAIS---REVKAMAS 66
 DB 38 PELSETETTESITLDGSGFGYVYKRCRL--KDPVAVMLKQVDKTLDFRREVALINSK 95
 QY 67 LDNEFYLRLEGVIEKVNMDQPRPALVTKFMENGLSGLLOSOCPRPWLRLKLEVYL 126
 DB 96 IFRPNVLTGLACTST-----PKMLICETELKGNLESLLDPMVKLPLTRMMAMADAL 151
 QY 127 GMFYLTLDQAPVLLHRLDKPSNVLPPELHVKLADFGSTF--QGSQSGSGSGSGPGTGLY 185
 DB 152 GYVIMLHSSNPVFIHNDLTKSNLYDANLTVAVCFGLSGLKQKQENLKKQDQCAKSTPLM 211
 QY 186 LAPELFEVN--VNRKASTMSDVYSGITLMAVLAERELETPESL--VTEAVCNRONRPS 241
 DB 212 MAEYVLOGRLFEKKA-----DVSFGLVLMQFTQREL--FEFNFNFRFAALICEKOLRPS 266
 QY 242 LAELPACGETPGLGELKELMLQNLSSSEPKRPSFOR-----CLPKTDEVFM 289
 DB 267 ---IPDCKRS-----LRELIOKMDPMEVPRPSEFEGVSELEIITIDCIP--DEYGA 316
 QY 290 V-----ENNMAAVSYTKDEL-----OLKSSNRFGITPESGOGGTENGFRTIE- 335
 DB 317 LKRNHFKHNEAN-----WKDTINFSNFGVGLTANRP--SKSDLDLPSPRLMG--STIEL 368
 QY 336 -----NOHSRNDVMSSEMLAKL---NLEPPSSVPRKCPSLTKRSRAQEE 377
 DB 369 NFKCLKSIIVSSPKGPHEEVVLMQPFCKVLAMPGNLKEGDSQILDKIRQL----- 419
 QY 378 QVPOARTAG--TSSDSMAOPROTPESTF 404
 DB 420 -MECAFHGDISTSESENRLKQKPE-GTF 446

RESULT 10
 Q9SR87 PRELIMINARY; PRT; 693 AA.
 AC Q9SR87; 01-MAY-2000 (TREMblrel. 13; Created)
 DT 01-MAY-2000 (TREMblrel. 13; Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19; Last annotation update)
 DE PUTATIVE SERINE/THRONINE PROTEIN KINASE.
 GN T16011.20.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID-3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Bonning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC T16011 genomic sequence."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBS databases.
 CC -1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AL30871; BAF07845.1.
 DR HSSP: P13306; ILDE.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR001220; Lectin_leg8.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR Pfam: PF00139; Lectin_leg8.1.
 DR Pfam: PF00069; pkinase.1.
 DR SMART: SM00221; STYK.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 693 AA; 77600 MW; 0EDB08A0303D5E4A CRC64;

Query Match 12.0%; Score 333; DB 10; Length 693;
 Best Local Similarity 30.5%; Pred. No. 1.6e-17;
 Matches 101; Conservative 71; Mismatches 115; Indels 44; Gaps 15;

QY 16 VSIELNDELNGKDGCGTFRPAQHRKRGYDVAVKI-----REVKAMASLDN 69
 DB 363 LATKFESEIITGCGFYVYKNGNLSGSG--PIAVKITNSLQGVREFMAIESIGRLGH 421
 QY 70 EFVRLLEGVIEKVNMDQPRPALVTKFMENGLSGLLOSOCPR-----PPLLCRLKE 123
 DB 422 KNIYVNGCKKHNN-----ELLITDYIPNGLSDSLY--QFRRNGIYLPMDVFEIIGK 475
 QY 124 VYLGFTLHQQ--NPVILHRLDKPSNVLPPELHVKLADFGLS--TQGSQSGTSGSGPG 181
 DB 476 IASGLTLHEHMQVYHVDVPSNVLLDQDNKAKLDGELARLEKTL--TOTTKIVG 533
 QY 182 TLGYLAPLEFVNVRKASTASDVYSGITLMAVLAERELETPESLYEA--VCNRON 238
 DB 534 TLGYMABEL--FRNGSGTASDVAFVGLLEIVCGNK---PTNNEFPLADVMEHRTN 588
 QY 239 RPSLAEPLQ-AGETPGLGELKELM--QICHSEPKDRPSF-----OCLPKTDEV 286
 DB 589 GGLTCYVDQNLSSFPKREARIALVGLLCHOKPFRPSMNVTLRIKNGSENVPOIDEN 648
 QY 287 EQVYENNNMAAVSYTKDELSSNRPS 316
 DB 649 WGFSDSRDCKSNVGVYSSDRASSSTPS 679

RESULT 11
 Q9H1Y7 PRELIMINARY; PRT; 564 AA.
 AC Q9H1Y7; 01-MAR-2001 (TREMblrel. 16; Created)
 DT 01-MAR-2001 (TREMblrel. 16; Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19; Last annotation update)
 DE D1662P8.3 (SIMILAR TO NAF310 (MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10)) (FRAGMENT).
 GN D1662P8.3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hall R.;
 RA Submitted (MAY-2000) to the EMBL/GenBank/DBS databases.
 RL EMBL: AL33380; CAC17571.1;
 DR HSSP: P06241; ISHF.


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DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50002; SH3; 1.
DR ATP-binding; Kinase; Transferase.
FT NON_TER 564 564
SQ SEQUENCE 564 AA; 62400 MW; DAFL9LE14842E7EB CRC64;

Query Match 11.7%; Score 324.5; DB 4; Length 564;
Best Local Similarity 26.5%; Pred. No. 5.4e-17;
Matches 130; Conservative 70; Mismatches 185; Indels 103; Gaps 21;

QY 8 PSQAPAP-----LVSEELLENQELVGRGEGTFVRAOHRK-GYDAVAVIV----- 53
DB 102 PAASPAAPPSPSPVHVAFERLELEKELIGAGFGGYVRA---TWQGEVAVAAARQDE 158
QY 54 -----SKAIREVKAMASLDNEFVLRLEKLVKVMNDQPKALVYTKFKENGSLGGLQ 107
DB 159 QDAAAASVRRARLPAHLRHPNITELRGCL-----QDPHLCLVLEFRAGALRALA 213
QY 108 SCQPRPAP-----LTCRLLEEVYLCMTLHDQNPV-LLRDLKPSNVLDP 152
DB 214 AANAADPPRAPGRARRIRPRLVYMAVQALRGMLTLHEAVRPLHLRDLKSSNILL 273
QY 153 ELH-----VLADFGSLSTFGSGSGSGSGEGTGLTAPLPELVYNNRKASTASDV 204
DB 274 KIEHNDICNKTJKTIDFGFLAR---EMHRTIKMSTAGTYAMNAPE-VIKSLIFSGSDI 327
QY 205 YSGGILMAVLAAGREVELTER-----SLVYAVCNRRNRSLAEFLQAGPEPGLGLEKE 260
DB 328 WSTGVGLMELTGS---EYVYRGIDGLAVAVYAAVNAKTLTP---IPSTCEP-----PAK 375
QY 261 LMDLCNSESSEKDRPSFOECLPR-----TDEPVQVNNNAVAVSTVKDFL--- 305
DB 376 LMECHQDQPHIRSPFALILEQALIECAVYNTKMPQSPHSMDMKLEIQMFDLRTK 435
QY 306 -SOLKSNRRFSIPESGCGCTEMDGFRTTNGHSRNDVAVSEKN-----KLTSEPPSS 360
DB 436 EKESRSEBELTAALQCSQSEELKRRQDLAREIDVLERE-LNLIFFOLNCKEPK-- 492
QY 361 VPKCPSLTKRSRAOEVOYPOAMTAGTSSD-----SMAOPQTPETSTERNQSPSTSG 415
DB 493 -VKKRRKGKFKRSRL--KIKDGRISLSPDQHKITQVQASPNDKRRSLNSSSSPSPSS 548
QY 416 TSPGPGRNG 425
DB 549 TMDPRLRAIG 558

RESULT 12
Q9M3D7 PRELIMINARY; PRT; 667 AA.
AC Q9M3D7
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RECEPTOR-LIKE PROTEIN KINASE.
GN F18N11.180.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsie.

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OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Jordan N., Bangert S., Wiedemann R., Voss H., Unsel N., Mewes H.W.,
RA Lemcke K., Mayer R.F.X., Queller F., Salanoubat M.;
RL Submitted (MDV-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (TEB-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AL132933; CAB72491.1; ..
DR HSSP: P02870; ILEN.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001220; Lectin_legB.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00139; Lectin_legB; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00221; STYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 667 AA; 74097 MW; 65F2P83FD4A26DBF CRC64;

Query Match 11.6%; Score 321.5; DB 10; Length 667;
Best Local Similarity 32.5%; Pred. No. 1.2e-16;
Matches 103; Conservative 48; Mismatches 113; Indels 53; Gaps 14;

QY 26 LVGDGEGTFVRAOHRKMGDYDAVAVIV-----SKAIREVKAMASLDNEFVLRLEGYI 79
DB 355 LVGGGEGGKYYKGR-LPGGRHIAVVKRLSHDAGQMKGFVAEYVTNGVIGRNLVPLGYC 413
QY 80 EKVYNDQDPKALVYTKFKENGSLG-LLOSQPRP-NPLCLRLKEVYLCMTLHD-ONP 136
DB 414 RRGK-----ELLVSEKNGSLDQYLPYONPSPSWLQRIIILKADASLNTLHSGANP 468
QY 137 VLHRDLKPSNVLDPPELHVKLADFGSLSTFG--QSQSGSGSGEGTGLTAPLPELVN 194
DB 469 AVLHRDLKASVNLDSYNGRLGDFQMAKFPDPQGNLSATPA---VGTIYMAPEL---I 522
QY 195 NRKASTASDVYSFGIILMAVLAGR---EVELPTBPSLVYAVCNRRNRPSIAEL--PQAG 249
DB 523 RTGSKETDVTYAGITFLLEVTCGRNRPFEELPVQKKIYKVCCHQASLLTTRDPKIG 582
QY 250 PE--TPGLGIAELMDLCNSESSEKDRPSFOECLPRXTDEVQVNNNAVAVSTVKDFLSQ 307
DB 583 REFLSEVEVYLCMTLCTNDVPSRPD-----NGOVMOYLSQ 620
QY 308 LKSNRRFSIPESGCG 324
DB 621 -KQPLPDPFSADSPGIG 636

RESULT 13
Q9M020 PRELIMINARY; PRT; 668 AA.
AC Q9M020
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RECEPTOR LIKE PROTEIN KINASE.
GN F7A7.70.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]

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OC eucroide II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
 RA Lee J.M., Onodera C.S., Ouach H.L., Tang C., Toriumi M., Wu H.C.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Koeseema E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.O., Sakurai T., Satou M., Seki M.,
 RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RT *Full Length cDNA of gene At1g67890 (GI:15220577).
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY059769; AAL24117.1;
 KM Hypothetical protein.
 SO SEQUENCE 765 AA; 65149 MW; 6651738FBAE347D4 CRC64;

Query Match 11.5%; Score 318.5; DB 10; Length 765;
 Best Local Similarity 34.4%; Pred. No. 2.4e-16;
 Matches 98; Conservative 41; Mismatches 101; Indels 45; Gaps 11;
 QY 19 EELENOELVGDGFGTVPRAQHRK-GYDAVAVIKNSKAIS-----REYKAMASLDN 69
 Db 485 EDLTNGEOIGGSGCTVY---HGLMFGSDVAVKVFSSKEVSEETISFKQEVSLMKRLRH 541
 QY 70 EFYLRLECIEKVMNDQPKRALYTKPMENSGLSGLQ--SGCPRPPLCLRLKEVYLG 128
 Db 542 PNYLTFMGAVA-----SPQRLCTVETFLPQSLERFLQNNKSKLDLRRRIHNASDIARGM 596
 QY 129 FYLADQNPVLLRDLPKSNVLPPELHVKLADPQLSTFGGSGSGTSGSGEGGTLGYLAP 188
 Db 597 NYLHRCSPPIIHRDKSSNLLVDRMWTYKADFGLSRIKHETYLTLTNG---RGTPOMMAP 653
 QY 189 ELFVNVRKASTASDVYSFGILMAVLAGREVELTEPSLVYEAVCNCRQNPRLAELPQA 248
 Db 654 E--VLNENAADEKSDVYSGVYLM-----ELVTE-KIPWE-----NLNAQVIGAV 696
 QY 249 GPRTPLGLEKLE-----LMQLCMSSEPRDRPSFOCLPKTDEY 286
 Db 697 GPNQRLVYKDVDPQWITALMESCHWSEPCQRPSPFOELNDKLEL 741

Search completed: August 13, 2002, 22:14:15
 Job time: 462 sec

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 13, 2002, 22:08:18 ; Search time 24.11 Seconds
(without alignments)
633.490 Million cell updates/sec

Title: US-09-762-491-6
Perfect score: 2774
Sequence: 1 MSCKLWPSGAPALVISE.....PRODEANSRQGCWYNSGRZ 519

Scoring table: BLOSUM62
Gapop 10.0 , Capopt 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445.5	16.1	656	1 RIP_MOUSE	Q06855 mus musculu
2	423	15.2	671	1 RIP_MOUSE	Q13546 homo sapien
3	401	14.5	832	1 ANR3_HUMAN	P57078 homo sapien
4	321	11.6	606	1 M3K7_HUMAN	O43118 homo sapien
5	312.5	11.3	579	1 M3K7_MOUSE	O62073 mus musculu
6	303	10.9	954	1 M3KA_HUMAN	O02779 homo sapien
7	302	10.9	821	1 CTR1_ARATH	O05609 arabidopsis
8	295.5	10.7	628	1 TESK_RAT	O63772 rattus norv
9	294.5	10.6	513	1 AVR2_SHEEP	O28660 ovis aries
10	292.5	10.5	513	1 AVR2_RAT	P38444 rattus norv
11	290.5	10.5	513	1 AVR2_BOVIN	Q28043 bos taurus
12	290.5	10.5	513	1 AVR2_HUMAN	P27037 homo sapien
13	290.5	10.5	513	1 AVR2_MOUSE	P27038 mus musculu
14	287.5	10.4	394	1 M3K9_HUMAN	P80192 homo sapien
15	286.5	10.3	514	1 AVR2_XENLA	P27039 xenopus lae
16	286.5	10.3	902	1 EPBR_XENLA	O91736 xenopus lae
17	285.5	10.3	984	1 EPB1_HUMAN	P54762 homo sapien
18	285.5	10.3	984	1 EPB1_RAT	P09759 rattus norv
19	285	10.3	974	1 EPB3_XENLA	O91735 xenopus lae
20	283	10.2	1051	1 URK1_MOUSE	O70405 mus musculu
21	282	10.2	976	1 EPB2_HUMAN	P29317 homo sapien
22	281	10.1	888	1 M3KC_MOUSE	O60700 mus musculu
23	279.5	10.1	904	1 EPB1_CHICK	O07494 gallus gall
24	276.5	10.0	501	1 KPEL_DROME	O05652 drosophila
25	276.5	10.0	512	1 AVR8_BOVIN	O95126 bos taurus
26	276.5	10.0	512	1 AVR8_HUMAN	O13705 homo sapien
27	276	9.9	901	1 CR14_MALZE	O24585 zea mays (m
28	276	9.9	1004	1 EPB2_CHICK	P26893 gallus gall
29	275.5	9.9	986	1 EPB1_HUMAN	P21709 homo sapien
30	275	9.9	888	1 M3KC_RAT	O63796 rattus norv
31	273.5	9.9	977	1 EPB2_MOUSE	O03136 mus musculu
32	273.5	9.9	1055	1 EPB2_HUMAN	P29323 homo sapien
33	273.5	9.9	981	1 EPB3_HUMAN	O13146 brachydanio

34	273	9.8	987	1 EPB2_COTJA	O90344 coturnix co
35	273	9.8	1308	1 EPB4_HUMAN	O15303 homo sapien
36	272.5	9.8	536	1 AVR8_MOUSE	P27040 mus musculu
37	272.5	9.8	1520	1 ABL_DROME	P00522 drosophila
38	272	9.8	746	1 ABL_MOUSE	P00521 abelson mur
39	272	9.8	993	1 EPB2_MOUSE	P54763 mus musculu
40	271.5	9.8	354	1 KHOS_MSVMT	P32593 moloney mur
41	271.5	9.8	374	1 KHOS_MSVMO	P00398 moloney mur
42	270.5	9.8	630	1 TBC_MOUSE	P24604 mus musculu
43	270.5	9.8	1002	1 EPB5_CHICK	O07497 gallus gall
44	270	9.7	382	1 AVR8_RAT	P38445 rattus norv
45	270	9.7	859	1 M3KC_HUMAN	O12852 homo sapien

ALIGNMENTS

RESULT	ID	STANDARD	PRT	656 AA.
1	RIP_MOUSE			
AC	Q06855:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Serine/threonine protein kinase RIP (EC 2.7.1.-) (Cell death protein			
DE	RIP) (Receptor interacting protein).			
GN	RIP1 OR RIP OR RIMP.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid:10090;			
RP	[1]			
RC	SEQUENCE FROM N.A.			
RX	STRAIN-C57BL/6 X CBA; TISSUE-Thymus;			
RX	MEDLINE-95277838; PubMed-7538908;			
RA	Stanger B.Z., Leder P., Lee T.-H., Kim B., Seed B.;			
RT	*Rip: a novel protein containing a death domain that interacts with			
RT	Fas/Apo-1 (CD95) in yeast and causes cell death.*;			
RL	Cell 81:513-523(1995).			
CC	-1- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND			
CC	INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-			
CC	DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.			
CC	-1- TISSUE SPECIFICITY: FOUND AT LOW LEVELS IN ALL TISSUES.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: U25995; AAB60487.1; -			
DR	HSSP: P1362; JAGW.			
DR	MGD: MGI:108212; RRP1.			
DR	InterPro: IPR000488; Death.			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR004040; STY_pkinase.			
DR	InterPro: IPR002290; Ser_thr_pkinase.			
DR	Pfam: PF00531; death. 1.			
DR	Pfam: PF00069; pkinase. 1.			
DR	SMART: SM00005; DEATH. 1.			
DR	SMART: SM00221; STYK. 1.			
DR	PROSITE: PS00108; PROTEIN KINASE ST. 1.			
DR	PROSITE: PS50011; PROTEIN KINASE DOM. 1.			
DR	PROSITE: PS50017; DEATH_DOMAIN. 1.			
KW	Tnfrsfase; Serine/threonine-protein kinase; ATP-binding;			
KW	Apoptosis.			
FT	DOMAIN	17	290	PROTEIN KINASE.
FT	NP_BIND	23	31	ATP (BY SIMILARITY).
FT	BINDING	49	49	ATP (BY SIMILARITY).

FT ACT_SITE 138 138 BY SIMILARITY.
 FT DOMAIN 568 654 DEATH.
 FT VARIANT 473 473 T->I
 SQ SEQUENCE 656 AA: 74854 MW: ABB350B23879933 CRC64:

Query Match 16.1% Score 445.5; DB 1; Length 656;
 Best Local Similarity 26.2%; Pred. No. 2.6e-20;
 Matches 158; Conservative 89; Mismatches 205; Indels 151; Gaps 23;

15 LVSELENGEVLGKDGSTVFRAGHRKMGDVAVKIVN-----SKASREYKMAST 67
 DB MASSDLEETDL-DSGGGRKVSCLHSHGVIYAKTGTGNGRAETINIEBEGKMMRL 70
 QY 68 DNEFTVRLSG-VIEKVMQDOKPALVYKFMENGLSGLLQSCPPRPMLLCRLKEVYL 126
 DB 71 RHRVVKLLGIITIEGNY-----SLVMEYMKGNLHNVKTDIDVPLSKRITVEALE 124
 QY 127 GNFYLDONPVLLHDLKPSNVLPPPELHVRLADFGSLTFQGSQ-----SGT 174
 DB 125 GNCYLHDKG-VIHKDLKENILVDROFHILADLGAFTKNSKTLKEMDKOKEVST 182
 QY 173 GSGEPCGTGLYAPLPELVNVRKASTADYSGEILMAVLAGREVELPTEPSLYEAVG 234
 DB 183 TKNNKGTLYMAPPELNDINKPTKSDVSGEIVLALFAKKE--PYE-----NVIC 234
 QY 235 NMQ-----NPSLAEIPQAGPETPGLKELMQLCMSSEPKDRPSP---DECLPR 282
 DB 235 TEQFVICIKSNRPNVETIEECPRE-----IISLMERQALPEDEPFLGIEEFPRF 289
 QY 283 TDEVF-QVENVNNAVSTVNDFLSQLSKSRRFS-----IPES----- 320
 DB 290 YLSHFEEYEEDEV---ASLAKKETPPQSPVYLQRMESLQHDVCLPSPSSNSEQPSLHSG 346
 QY 321 --CGGTETMDQFRRIENQNSNDVMSYEMTK-----LNL 354
 DB 347 GLQMGVSEMSISSPEPPODENBSVAKQLEBASVHAFICAEIKQKRPQPNQNEAYVR 406
 QY 355 EEPSSVPRKPSLTNRKRAQEEVQPMATG-----TSSDMAQPPOTPEYST-FRNG 407
 DB 407 EERKRRVSHDPFOORAR---ENIKSAGARGHSDPSTSGIALVQOLSPATQTVWNG 463
 QY 408 MESPSTGTSPSPGPGNCAEKGKNNMSCRPEN-----PYTGRLPVN-----LY 453
 DB 464 LYNQGFQGTGCVVYPRNLGQNTSTYTPVPEINIGSGPFPYSGVADDLKTYTF 523
 QY 454 NCSGVQVGNNTLYMQOTTLPTKGLASGGRQLQHPVYSGQEGKPKDEANSPQCHY 513
 DB 524 NSSGIDIGHNTMDV-----GLNSQPPNNTCK---EESTSRQALTF 561
 QY 514 NNS 516
 DB 562 DWT 564

RESULT 2
 ID RIP_HUMAN STANDARD: PRT: 671 AA.
 AC 013546: 013180:
 DT 01-NOV-1997 (rel. 35, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Serine/threonine protein kinase RIP (BC 2.7.1.-) (Cell death protein
 DE RIP) (Receptor interacting protein).
 GN RIP1 OR RIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1:taxid:9606;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC TISSUE=umbilical vein endothelial cells;
 RX MEGINTE-96200892; PubMed-8612133;

RA Hsu H., Huang J., Shu H.-B., Balchwal V.R., Goeddel D.V.;
 RT "TNF-dependent recruitment of the protein kinase RIP to the TNF
 RT Receptor-1 signaling complex.";
 RT Immunity 4:387-396(1996).
 RL (2)
 RN REVISION TO 120.
 RP
 RA Hsu H., Huang J., Balchwal V.R., Goeddel D.V.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 300-671 FROM N.A.
 RX MEDLINE-95277838; PubMed-7538908;
 RA Stenger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
 RT RIP: a novel protein containing a death domain that interacts with
 RT Fas/Abd-1 (CD95) in yeast and causes cell death.";
 RL Cell 81:513-523(1995).
 CC -1- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND
 CC INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFRI IN A TNF-
 CC DEPENDENT PROCESS. REQUIRED FOR TNFRI ACTIVATION OF NF-KAPPA B.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC or send an email to license@sib.ch).
 CC
 CC EMBL: U50062; AAC32232.1;
 DR EMBL: U25994; AAC50137.1;
 DR HSSP: P1362; JAGW.
 DR MIM: 601453;
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR004040; Ser_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00531; death.1.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PRO0109; TYRKINASE.
 DR SMART: SM00005; DEATH.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS50017; DEATH_DOMAIN.1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Apoptosis.
 KM
 FT DOMAIN 17 289 PROTEIN KINASE.
 FT NP_BIND 23 31 ATP (BY SIMILARITY).
 FT BINDING 49 49 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DOMAIN 583 669 DEATH.
 FT DOMAIN 411 414 POLY-ARG.
 FT CONFLICT 514 514 T->S (TM REF. 3).
 SQ SEQUENCE 671 AA: 75958 MW: BADCE7E70456ABE CRC64:

Query Match 15.2% Score 423; DB 1; Length 671;
 Best Local Similarity 25.3%; Pred. No. 6.5e-19;
 Matches 145; Conservative 95; Mismatches 186; Indels 146; Gaps 22;

17 SIELENGEVLGKDGSTVFRAGHRKMG-----YDVAKIVNSKAIKREYKAAASIDN 69
 DB 14 SSDLESAEL-DSGGGRKVSCLFHRTGGLIMTKYVGPICIEHNNALLKAKNNRRRH 72
 QY 70 EYVRLGCVTEKVMQDOKPALVYKFMENGLSGLLQSCPPRPMLLCRLKEVYLVNF 129
 DB 73 SRVYKLGVI-----IEEKYSLVMEYMKGNLHNVKTDIDVPLSKRITVEALE 127
 QY 130 YLDONPVLLHDLKPSNVLPPPELHVRLADFGSLTFQGSQ-----SGTSGS 177
 DB 128 YLHCKG-VIHKDLKENILVDROFHILADLGAFTKNSKTLKEMDKOKEVST 184

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OY 178 EPGGILGYLAPLPELVNNKRASTADSVTSGILMAVLAGREVELPTEDSLYEAVCNQ 237
OY 185 NGSTLYNNAPEHNDVNNKPTREKSDVSPFVNLMAIPAKE---EYE-----MAICEQQ 236
OY 238 -----NRPSTLAPLQAGPPTPCLEIKELMOLCWSSEPKRSPFOCLPTDDEVRO- 288
OY 237 LINCISGNRPDVIDTECPRE-----IISMLKCHENAPPEARPF-----FOIEKRRP 287
OY 289 -----AVENNNNAVSTVQKDFLSQLSSNRR-----SIPSS----- 320
OY 288 FYLSQLEESVEEDVSKLREYSENAVNRKQSLDLCVAVPSSRSNATEQPSLHSSQ 347
OY 321 --GQGGETMDGFRRTIENOSHNDVSEWT-----NKLNLSEPPSVPKC 365
OY 348 GLGMPVEESMFAPSLFHPQENEPSTLQSLQDEANHYLGSRNDQTKQDPQNVAVNR 407
OY 366 PSLTKSRRAQEEVQPA-----WTAGTSSDSMAQ---PQTEPSTFRN 406
OY 408 EE-ERRRRVSHDPQAQRPYENFQTEKGTVYSSASHGNAVHOPGLTSGQFVLYONN 466
OY 407 QMPG-----PTSTGT-----PS-----PGRNGOAGEROGMNMSCTPER 441
OY 467 GLVSSHGFGFRPLDPETAGRVYWRPIPSHNPILNIFPETVYLGNTIPFSSILPFD 526
OY 442 NPVTGRPLVNYVNCGVGVGDNNYLTMOQTA 473
OY 527 ESIR-----YTIYNSITGIGAVNYMEIGTSS 554

RESULT 3
ANR3_HUMAN STANDARD; PRT; 832 AA.
AC P57078;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase ANKRD3 (EC 2.7.1.-) (Ankyrin repeat
domain protein 3) (PKC-delta-interacting protein kinase).
GN ANKRD3 OR DIK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-20289799; PubMed-10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totsuki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takegi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald A., Rump A., Schillabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minohama S., Shimizu N., Nordstam G., Hornischer K., Brandt P.,
RA Schafte M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
RA Remer J., Beck A., Klages S., Hennig S., Rieseemann L., Dagand E.,
RA Weinmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Ischack H., Reinhardt K., Tsapo H.-U.,
RT "The DNA sequence of human chromosome 21."
RL Nucleu 405:311-319(2000).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 10 ANK REPEATS.
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CC or send an email to licenses@sdb-sdb.ch).
CR EMBL: AF001743; BAA95526.1; -

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DR MIM: 603706; -
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR004040; STY_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00023; ank; 10.
DR Pfam: PF00069; kinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00248; ANK; 10.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS50088; ANK_REPEAT; 9.
KW transferase; serine/threonine-protein kinase; ATP-binding; Repeat;
KW ANK repeat.
FT DOMAIN 22 286 PROTEIN_KINASE.
FT REPEAT 485 514 ANK 1.
FT REPEAT 518 547 ANK 2.
FT REPEAT 551 580 ANK 3.
FT REPEAT 584 613 ANK 4.
FT REPEAT 617 647 ANK 5.
FT REPEAT 651 680 ANK 6.
FT REPEAT 684 713 ANK 7.
FT REPEAT 717 746 ANK 8.
FT REPEAT 750 780 ANK 9.
FT REPEAT 782 811 ANK 10.
FT NP_BIND 28 36 ATP (BY SIMILARITY).
FT BINDING 51 51 ATP (BY SIMILARITY).
FT ACT_SITE 143 143 BY SIMILARITY.
SQ SEQUENCE 832 AA; 91610 MW; 508FFED5F04F7EBCB CRC64;

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Query Match 14.5%; Score 401; DB 1; Length 832;
Best Local Similarity 28.4%; Pred. No. 1.9e-17;
Matches 126; Conservative 71; Mismatches 173; Indels 74; Gaps 14;
OY 10 GAPALVSI-----ELENDLVGKDGRTVFRQHRMKGTVDAVKVNSKAIS----- 58
DB 6 GTPALALLTFDAGETGTEWEGSGEGQYKVRHVMKTNLAIKSPSLHVDRENE 65
OY 59 --REVKKMASLNDPEFVLREGVLEKVNMDQPKPALVTKFENSGSLGLQSCPPMP 116
DB 66 LLEAKKREAKRRTIIPYVGICR-----PVGLVNVEKMGSTLEKLASE-PLPMDL 117
OY 117 LCRLLKEVYLGKFTLHDQNPVLIANDLKPSTVLPDPPLHVKLADFGISTFGSGSGTGS 176
DB 118 RFRTHETAVGNMFLCNAPPLHLDLKPANLIDAHYVNTISDFGLAKNGLSHSDLS 177
OY 177 GEP-GGTGLYLAPELVNNKRASTADSVTSGILMAVLAGREVELPTESLYEAV-C 234
DB 178 MDGLFGITAVLPERRIREKSRLEDFTRKHQVSPAIYIMCVLTQK-PRADKKNLHINVKY 236
OY 235 NRRPRLAELPQAGETGGLGELKELMOLCWSSEPKRSPFOCLPTDDEVQVNNNN 294
DB 237 VKGRPELPYCAARR--ACSHLRLMQRCHQSDPRVRPFPQ-----GNGL 281
OY 295 NAAVSTVKDFLSQLKSNRRFSTIPESGCGGTMDGFR-----RRT 334
DB 282 NGEL--TRQVLAAL-----LPVTGRNRSFGEGFRLESEVYIIRVTCPLSPQETTSR 331
OY 335 ENQSRNDVYSEWTLKLNLEPPSSVPAKCSILTKRSRA-----OEQVQPAWTAGTSSD 390
DB 332 EDLEKRPDDVETKATDLDVQKSPERSEVPARLKRAASATFDNDVSLSELLSDQSGV 391
OY 391 SMA-OPQPTETSTFNMOWSPRTS 413
DB 392 SQAVEGPEBELSRSSSESKLPSSGS 415

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RESULT 4

ID	MARK	HUMAN	STANDARD	PT:	606 AA.
AC	043318	043317	043319		
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Nitrogen-activated protein kinase kinase 7 (EC 2.7.1.-) (transforming growth factor-beta-activated kinase 1) (tgf-beta-activated kinase 1).				
GN	MAP3K7 OR TAK1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.				
RC	TISSUE=Lung:				
RX	MEDLINE=88153801; PubMed=9480845;				
RA	Sakurai H., Shigemori N., Hasegawa K., Sugita T.;				
RT	"tgf-beta-activated kinase 1 stimulates NF-kappa B activation by an NF-kappa B-inducing kinase-independent mechanism.";				
RL	Biochem. Biophys. Res. Commun. 243:545-549(1998).				
CC	-1- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKs. B MEDiator OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B ACTIVATION.				
CC	-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1A, 1B (SHOWN HERE) AND 1C; ARE PRODUCED BY ALTERNATIVE SPLICING.				
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE KINASE SUBFAMILY				
CC	-1- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO C21ORF7.				
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CC	OR SEND AN EMAIL TO license@isb-sib.ch).				
DR	EMBL; AB009357; BAA25026.1; -				
DR	EMBL; AB009356; BAA25025.1; -				
DR	EMBL; AB009358; BAA25027.2; -				
DR	HSP; P00523; 2PTR.				
DR	MIM; 602614; -				
DR	InterPro: IPR000719; Euk_kinase.				
DR	InterPro: IPR004040; ST_kinase.				
DR	InterPro: IPR002290; Ser_thr_kinase.				
DR	InterPro: P00069; Pkinase; 1.				
DR	SMART: SM00221; STYK; 1.				
DR	PROSITE; P500107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; P500108; PROTEIN_KINASE_ST; 1.				
DR	PROSITE; P550011; PROTEIN_KINASE_DOM; 1.				
KW	Transferase: Serine/threonine-protein kinase; ATP-binding; Alternative splicing.				
KW	DOMAIN	8	14	POLY-SER.	
FT	NP_BIND	36	291	PROTEIN KINASE.	
FT	BRIDING	42	50	ATP (BY SIMILARITY).	
FT	ACT_SITE	156	156	ATP (BY SIMILARITY).	
FT	VARSPIC	404	430	BI SIMILARITY.	
FT	VARSPIC	509	518	MISSING (IN ISOFORM 1A).	
FT	VARSPIC	519	606	PLAIPNSKE -> ARTSCRGPG (IN ISOFORM 1C).	
FT	VARSPIC	519	606	MISSING (IN ISOFORM 1C).	
FT	SEQUENCE	606 AA;	67196 MW;	3DBF8147CD174013 CRC64;	
Query Match	11.6%; Score 321; DB 1; Length 606;				
Best Local Similarity	26.6%; Pred. No. 1,1e-11;				
Matches 134; Conservative 77; Mismatches 182; Indels 110; Gaps 26;					
0y	11 APALVYSIE-----ELEENGLVKGDSFGVYFAOHKRM-GIDVAVKTVNS-----KAISNE 60				
0b	11 AFSVLLNFEIDKLEIVKGVGGAAVGVCA---KMRADVAIKIIESSERKATVE 77				

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Oy 61 VKAMSLDNEVLEGEV-LEKWNMDODPKPALYTKFMENGSLSGLSQCPRP----- 113
Db 78 LRQSLSVNHPRIYKILGACLNPF-----CLYMEVAREGSGLYNVLGAPDELYTAAH 129
Oy 114 ---WPLCEKLEKVVLYGMFYLDQNP-VLLRDLKPSN-VLPPELYKVLADRG-----LS 164
Db 130 AMSWLCQGS-----QGVAILHSMPKALIRDLKPRLLVAGVTLICDQFTACDIO 183
Oy 165 TEQGSQSGSGTSGCPGCTGLGAPELFYVNRKASTASDVYSGILMAVLAGREV--EL 222
Db 184 THHTNNK-----GSAAMAPEFEESN--YSEKCDVFSWCIILREVITRRKPPDEI 232
Oy 223 PREPPELYEAVCNQNRPSLAELPQAGETPGEGLELQWLCWSEPPDRSPQEC-- 280
Db 233 GGAAPRIMAAVHNHTRRPLKLNLPK-----ISLWTRKMSNDSPQRMSBELYKI 283
Oy 281 -----PKTDEVFQNV-----ENNNAAVSTYKDFLSQAKSNRRPSIPESQCGTEM 327
Db 284 MTHLMKTPGADPELOYPCYSDQGSNSATST--GSPFDIASTN-----TSKNSDTNM 335
Oy 328 DCFRRP-----IENQSRNDVAVSEMLKLNLEPPSSVPRKCP--SLTRRSBAQEQV 379
Db 336 EQVPATNPDTIRLESRLKKNQAKQSGSGRLSLDASGSSVSESLPTSGSRMSADHSEI 395
Oy 380 PQAKTRAGSSSSMAHQPPQETPERN--QWSPSTSPGTSPEPPRNGARQGMNSCR 437
Db 396 -EKRIATATASKRKGHR-KLSTGFNLIDPELYISGNGOPRRMSIDDLVTG----- 447
Oy 438 TPEPNPVTGR--PLVNIYWCSG 457
Db 448 -TEPGOVSRSSSPVNRMITTSG 469

RESULT 5
M3K7_MOUSE
ID M3K7_MOUSE STANDARD; PRT: 579 AA.
AC 062073:
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Mitogen-activated protein kinase kinase 7 (EC 2.7.1.-)
DE (transforming growth factor-beta-activated kinase 1).
DE activated kinase 1).
DE MAPK7 OR TAK1.
GN MAPK7 (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090:
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=9613277; PubMed=8533096;
RA Yamaguchi K., Shirakabe K., Shibuya H., Ito K., Ohnishi I., Ueno N.,
RA Taniguchi T., Mishida E., Matsuno K.;
RT Identification of a member of the MAPKK family as a potential
RT mediator of TGF-beta signal transduction.*
RL Sequence 270:2008-2011(1995).
CC -1- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKs.
CC ACTIVATOR OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B
CC ACTIVATION.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION, STRONG, TO C10AP7.
CC -----
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CC -----
CC EMBL: D76446; BA01104.1; -.
CC HSSP: P12931; IPRK.

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DR MKD; MG1:1346877; MAP3K7.
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR004040; STY_pkinase.
 DR Interpro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00221; STYKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR Transferase: Serine/threonine-protein kinase; ATP-binding.
 KW DOMAIN 8 16 POLY-SER.
 FT DOMAIN 36 291 PROTEIN KINASE.
 FT NP_BIND 42 50 ATP (BY SIMILARITY).
 FT BINDING 63 63 ATP (BY SIMILARITY).
 FT ACT_SITE 156 156 BY SIMILARITY.
 SO SEQUENCE 579 AA; 64227 MW; 97CB6F3CB8283EE CRC64;

Query Match 11.3%; Score 312.5; DB 1; Length 579;
 Best Local Similarity 25.4%; Pred. No. 3,4e-12;
 Matches 126; Conservative 77; Mismatches 170; Indels 123; Gaps 24;

QY 11 APAPVLSIE-----ELENDLVKDGCTVRAOHRKW-GYDAVAVKIVS---KAISRE 60
 DB 21 APSQVLMFEEDIOYKEIEVEYVGCAGFCVCKA---KRAKDAVIAKIQISESBRAKATVE 77
 QY 61 VKMAAGLGNFVLRLEGV-IEKVMNDOPKALVTNENHGSLSGLSOSCCRP----- 113
 DB 78 LROSLKRNHNYKLGACLNRY-----CLVMTABSGSLNVHGAEPPLPTTAAH 129
 QY 114 ---WPLLCRLKLEVYLGMEYLLHDNP-VLHARDKPSN-VLPPELRYVLADFC---LS 164
 DB 130 AMSMCILQCS-----OCVAYVLSHQPRLIHRDKLPNLLVAGGVLLICDFGTACDQ 183
 QY 165 TPQCGSGSGSGEPEGTGLVAPLPELVNVRKASTADYVSFGIIMVAVIAGREV--EL 222
 DB 184 THRTNKK-----GSAAMAPVEFGSN--YSEKCDVFSNGITIMETVIRKRPDEI 232
 QY 223 PTEPSLYTEVNCNRNRPSELAPAGETGCLGELKELMQLVSSBPDRPSPOBCL-- 280
 DB 233 GGAPRALMVAHNGTRPPLIKLPP-----ISLWTRKWSMDPQRPBMEIYKI 283
 QY 281 -----PKTDEVFQNV-----ENNNNAVSTVKDELSQLKSNRFRSIPESGOGTEEM 327
 DB 284 MTHLMRYFPADDEPLQYPCOYSDGOSNATST-----GSPM 320
 QY 328 DCFRRRTIENOHSHNDVNVSEMLNKLNEPPSS--VPRKCPSLTKRSRAOEGVQAWTA 385
 DB 321 D-----IASNTSK-----SDPMQGVATNDITIKLESLKLNQAKQSSBGRSL 368
 QY 386 GTSSDSMAOPQOTPETSTFRNQHSPSTGTGPPGPRGN-OGAEKQGMNMSCRTPPNPV 444
 DB 369 GAARGSSVE--SLPPTSEGRMSADMSIEARIVATAGNGQPRRSIODLVGTGTEPGOV 426
 QY 445 TGR---PLVNIYWCSC 457
 DB 427 SSRSSPSVAMNITSG 442

RESULT 6
 MKAL_HUMAN STANDARD; PRT; 954 AA.
 ID MKAL_HUMAN 002779; 012761; 014871;
 AC 01-FEB-1994 (Rel. 28; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Mitogen-activated protein kinase kinase kinase 10 (EC 2.7.1.37)
 DE (Mixed lineage kinase 2) (Protein kinase MST).
 GN MAP3K10 OR MKK OR MST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;

RM [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96128179; PubMed=8536694;
 RA Dorew D.S., Devereux L., Tu G.F., Price G., Nicholl J.R.,
 RA Sutherland G.R., Simpson R.J.;
 RT "Complete nucleotide sequence, expression, and chromosomal
 RT localisation of human mixed-lineage kinase 2.";
 RL Eur. J. Biochem. 234:492-500(1995).
 RM [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95249256; PubMed=7731697;
 RA Kato M., Hirai M., Sugamura T., Terada M.;
 RT "Cloning and characterization of MST, a novel (putative)
 RT serine/threonine kinase with SH3 domain.";
 RL Oncogene 10:1447-1451(1995).
 RM [3]
 RP SEQUENCE OF 244-480 FROM N.A.
 RC TISSUE=Colon epithelium;
 RX MEDLINE=9328756; PubMed=8477742;
 RA Dorew D.S., Devereux L., Dietzsch E., de Kretser T.;
 RT "Identification of a new family of human epithelial protein kinases
 RT containing two leucine/isoleucine-zipper domains.";
 RL Eur. J. Biochem. 213:701-710(1993).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKELETAL MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; X90846; CA62351.1; -;
 DR EMBL; X46615; CA68531.1; -;
 DR PIR; S2468; S32468.
 DR HSSP; P29355; ISEM.
 DR MIM; 600137; -;
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR001452; SH3.
 DR Interpro: IPR004040; STY_pkinase.
 DR Interpro: IPR002290; Ser_thr_pkinase.
 DR Interpro: IPR001245; TYR_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00221; STYKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00002; SH3; 1.
 KW Transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KW ATP-binding; SH3 domain.
 FT DOMAIN 2 5
 FT DOMAIN 16 81
 FT NP_BIND 98 360
 FT BINDING 104 112
 FT ACT_SITE 125 125
 FT ACT_SITE 222 222
 FT DOMAIN 384 405
 FT DOMAIN 419 440
 FT DOMAIN 449 463
 FT CONFLICT 462 464
 FT CONFLICT 465 480
 FT REF. 3);
 LKLEGGSHISPSGF -> AQAAAGRRPHPALTL (IN


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FT      MOTAGEN      694      694      TREATED PHENOTYPE.
FT      SEQUENCE      821 AA: 90306 MW: 292203DCDDCC15BC CRC64:
SQ
Query Match      10 98: Score 302; DB 11; Length 821;
Best Local Similarity 33.68; Pred. No. 2.3e-11;
Matches 92; Conservative 44; Mismatches 96; Indels 42; Gaps 12;

OY 20 ELENQELVGEKDGFGVFRQHRK-GYDVAVKYNSK-----AISREVMASLDNE 70
DB 550 DLNKKIKGSGSGYVRAE---WEGSDVAVKILMEDQFAEVRNEFLREVMIRLHNP 606
OY 71 FVRLGVEIEKVMDDPPALVTKFENSGLSGLSQCPRRPPLLCRLK---EYVIG 127
DB 607 NIYLFPGAV-----TQPMILSYTEYLSRGLYRLHLSKARQDLDERRLMAVDVAKG 661
OY 128 MFTLHQNPVLLHRLDKPSNVLPPDELHVKLADFGLSFGGSGSGSGSGGEGTLYLA 187
DB 662 MNYLHNRNPPIVHRLDKSPNLLVDKRYVVCDFGLSRK--ASTLSKSAAGTPEWMA 719
OY 188 PELFVNNKASTADVYSFGILMAVLAGREVELPEPELVYEAU---CNQNPISLAE 244
DB 720 PE--VLRRPSPKSDVYSFGVILMELATLQCPMGCNLNPQVVAAGFCRKR-----LE 771
OY 245 LRP-AGPPTPG-LBGLKELMQLCSSEPKORPSF 276
DB 772 IPRNLNPVAAITBQ-----CMTNEPKRPSF 798

RESULT 8
TEST_RAT
ID TEST_RAT STANDARD: PRT: 628 AA.
AC 063572:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Testis-specific protein kinase 1 (EC 2.7.1.1).
GN TESTK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID:10116;
RN 1)
RP SEQUENCE FROM N.A.
RC STRAIN-NISTAR: TISSUE-Testis;
RX MEDLINE-96125123; PubMed-8537404.
RA Yoshida J., Ohashi K., Okano I., Nunoue K., Kishioh M., Kuma K.-I.,
RA Miyata T., Hirai M., Baba T., Mizuno K.;
RT Identification and characterization of a novel protein kinase,
RT TESTK, specifically expressed in testicular germ cells."
RL J. Biol. Chem. 270:31331-31337(1995).
CC -1- FUNCTION: DISPLAYS SERINE/THREONINE-SPECIFIC PHOSPHORYLATION OF
CC MYELIN BASIC PROTEIN (MBP) AND HISTONE IN VITRO. PROBABLY PLAYS A
CC CENTRAL ROLE AT AND AFTER THE MEIOTIC PHASE OF SPERMATOGENESIS.
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN TESTICULAR GERM
CC CELLS.
CC -1- DOMAIN: THE EXTRACATALYTIC C-TERMINAL PART IS HIGHLY RICH IN
CC PROLINE RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: D50864; BAA09460.1;
DR HSP: P11362; LAGY.
DR InterPro: IPR000719; Euk_pkinase.

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DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KM Transferrase; Serine/threonine-protein kinase; ATP-binding.
FT NP_BIND 52 310 PROTEIN KINASE.
FT NP_BIND 58 66 ATP (BY SIMILARITY).
FT BINDING 71 71 ATP (BY SIMILARITY).
FT ACT_SITE 170 170 BY SIMILARITY.
SQ SEQUENCE 628 AA: 67987 MW: 70567 FMD934B9AD CRC64;

Query Match      10 78: Score 295.5; DB 1; Length 628;
Best Local Similarity 23.38; Pred. No. 4.1e-11;
Matches 133; Conservative 82; Mismatches 213; Indels 143; Gaps 25;

OY 11 APAPVSIIELENOELVGDGFGVFRQHRKGYDVAVKI---VNSKAISREVMAS 66
DB 42 AVSSILARVDPDFCAEKIGAGFSEYKVRHRQSGVAVLKMNLPSRSNTLAEVDLMNR 101
OY 67 LDNEFVRLGVEIEKVMDDPPALVTKFENSGLSGLSQCPRRPPLLCRLKEVYL 126
DB 102 LRHNIIRFMGVCV---HGGQLHAL-TEYANGTLEGLSSPEPLSHVRLHLDLQ 156
OY 127 GMFTLHQNPVLLHRLDKPSNVL---PDELHVKLADFGLS---TFGGSGSGSGGEP 179
DB 157 GLRRLHAKG--VEHRLDTSKNCLYRREDGFTAVAGDGLAEKIPYREGARK-----EP 209
OY 180 GGTGSG--YLAPLFVN--VNNKASTADVYSFGILMAVLAGREVELPEPELVYEAUC 234
DB 210 LAVGSPYVMAPEVLNGELYDEKA---DVFAFGVLCETIA---RVADPDY----- 255
OY 235 NRRNPISLAEPLQAGPEPTGLSLKE-----LMQLCSSEPKORPSFOECLPTDE 285
DB 256 -----LPTDEFGLDVPAFTLVGNCPLPFLILAIHCCSNEPSARAPETITQHLEQ 308
OY 286 VFOVTEENMAAVSTYKDTLSQKSNRRPSIPESGGGEGTEMDGFRRTINQHSRDVAV 345
DB 309 ILELPEPTPLA---KPIIARAPLITINOGSVPRGGSAT-----LPRSDPL 352
OY 346 SEMNLKLTLEPPSVPRKCPSLJTK-----RSR 373
DB 353 SRSRSDLELPSPSPSPSMGMDLTVNPFSLREDLRGKIKLDTDPCKPATPLVLPSP 412
OY 374 AQEDQVQAMTAGTSSDSAP-----PQPTSTFRNQMPSTGTPSGCRPG 423
DB 413 LTSTQLPLV---ASPESLVQPEPTVPRCRSLPSPE-----LPRMETALPGFSP 461
OY 424 NQGAERGMNMSCRTEPPNVTGRPLVNIYNCSGVOYGDNNITLMOOTALPTMGILAPSG 483
DB 462 VGPSTERRMCEGSSPEPPAPQPLP-----AVATDNFISTCSSASOP-WSARP-- 512
OY 484 KGRGLDHPPP---VGSQEG-PRDPFASRPQ 510
DB 513 -GPSLANNPPAVYVNSPQSHARP--NNRAQ 540

RESULT 9
AVR2_SHEEP
ID AVR2_SHEEP STANDARD: PRT: 513 AA.
AC 028560;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
GN ACTR2 OR ACTRII.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.

```

OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ROMNEY; TISSUE=Ovarian follicle;
 RA Tisgall D.J.;
 RL Submitted (Mar-1996) to the EMBL/GenBank/DBJ databases.
 CC
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGF β RECEPTOR SUBFAMILY.
 CC
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 CC
 CC EMBL: L19442; AAA1903.1; -
 DR HSSP: P27038; 18RE.
 DR InterPro: IPR0000333; ActivinII_receptor.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF01064; Activin_rec_1.
 DR Pfam: PF00653; Pkinase_1.
 DR PRINTS: PR00653; ACTIVIN2R.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR Receptor: Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 513
 FT DOMAIN 136 161
 FT TRANSMEM 162 513
 FT DOMAIN 192 485
 FT NP_BIND 198 206
 FT BINDING 219 219
 FT ACT_SITE 322 322
 FT CARBOHYD 43 43
 FT CARBOHYD 66 66
 FT SEQUENCE 513 AA: 57768 MW: 731859585045783 CRC64;
 SQ
 Query Match 10.68; Score 294.5; DB 1; Length 513;
 Best Local Similarity 30.18; Pred. No. 3.7e-11;
 Matches 99; Conservative 56; Mismatches 125; Indels 49; Gaps 15;
 OY 12 PAPVLSIELENOELVGRDGFGRFAHNRMGVDVAVKIV-----NSKAISREYKAMAS 66
 DB 183 PSLPLGLAPDLGLEKAKGSGCYWKKMO--LNEYAVAKIKFFPIODKOSQONREYISLPG 240
 OY 67 LDNEFVLDEGVIEKVNMDOPKALYTKRNENSGSLGOSCPMPPLCLRLKEVYL 126
 DB 241 MNEHNLDTGIG-ERKGTGSVDYDLMTFAHKGSGSDFLKAVV--SMNELCIHAEIEMAR 298
 OY 127 GNEVYLD-----QNEFVLLDRKSNVLPPELHVYKLADGSLG--TFQSGSSGSGTSG 177
 DB 299 GLAYLHEPTIGLKDKGKRAISHRDIKSNVLLKNNLTACIADGGLAKLEAKSGADRHG 358
 OY 178 EFGGTLGLVLAPELF--VNVNRKASTASDVYSFGILNANVLGR-----EVELP-- 223
 DB 359 QV-GTKRRMAPEVLEGAINRQDAFLAIDHYAMGLVME--LMSRCIADGPDVEINLPEFV 416
 OY 224 ----TEPSL--VTEAVCKRONRPSLAELPQAGPEPTGLBLKELMQLCNSSPKRPSFQ 277
 DB 417 EEIGQHPSLDEMQEVVYHKKRPVLRDYNQ--KLGMKMLCETIEECWDHDAEARLS-A 472

OY 278 ECLPRTDEVQWVENNNNAVSTVDFLS 306
 DB 473 GCVCERTQKQRLFN-----ITTEDIVT 496
 RESULT 10
 ID AVR2_RAT STANDARD; PRT; 513 AA.
 AC P38444;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
 GN ACTR2 OR ACTRII
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
 RX MEDLINE=93279247; PubMed=7916681;
 RA Feng Z.M., Madigan M.B., Chen C.L.C.;
 RT "Expression of type II activin receptor genes in the male and female
 RT reproductive tissues of the rat.";
 RL Endocrinology 132:2593-2600(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=93050162; PubMed=1385212;
 RA Shinohara H., Ito I., Hasegawa Y., Nakamura K., Igarashi S.,
 RA Nakamura M., Miyamoto K., Eto Y., Ithuku Y., Minegishi T.;
 RT "Cloning and sequencing of a rat type II activin receptor.";
 RL FEBS Lett. 312:53-56(1992).
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGF β RECEPTOR SUBFAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: L10639; AAA0674.1; -
 DR HSSP: S48190; AAB23958.1; -
 DR HSSP: P27038; 18RE.
 DR InterPro: IPR000333; ActivinII_receptor.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF01064; Activin_rec_1.
 DR Pfam: PF00653; Pkinase_1.
 DR PRINTS: PR00653; ACTIVIN2R.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR Receptor: Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 513
 FT DOMAIN 136 161
 FT TRANSMEM 162 513
 FT DOMAIN 192 485
 FT NP_BIND 198 206
 FT BINDING 219 219
 FT ACT_SITE 322 322

FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 165 165 M -> K (IN REF. 2).
 FT CONFLICT 218 218 V -> I (IN REF. 2).
 FT CONFLICT 353 353 G -> A (IN REF. 2).
 FT CONFLICT 475 475 L -> V (IN REF. 2).
 SO SEQUENCE 513 AA: 57892 MW: C63A8742EF91DD7D CRC64;

Query Match 10.5%; Score 292.5; DB 1; Length 513;
 Best Local Similarity 29.8%; Pred. No. 4.9e-11;
 Matches 98; Conservative 55; Mismatches 127; Indels 49; Gaps 14;

12 PAPVLSIELENOELVGKDGFTVRAQHRKGVDAVKIV-----NSKAIISREVKAMAS 66
 DB PSLPLGKLPQLLEVKARGRFCGVMAQ--LLNEVAVAKIPIPDQKSMQNEVEVYSLPG 240
 QY 183 PSLPLGKLPQLLEVKARGRFCGVMAQ--LLNEVAVAKIPIPDQKSMQNEVEVYSLPG 240
 QY 67 LDNEVFLRLEGVIERVKNQDPRPALVTKFMENSGLSGLDSOCPRPPLCLRLKEVYL 126
 DB 241 MKHENILOFIGA-EKRGTSVDVDMLTITAFHEKGLSDPLKANYV-SMNEICHIATETMAR 298
 QY 127 GMFYLD-----ONPVLLHRDLKPSNVLPDEPLHVKLADFGLS-TFQGSQSGTSGS 177
 DB 299 GLAVLHEDIPGLKDGHRPAISHRDIKSKVLLKNNLFCIADFLALFKPAGKSGDTHG 358
 QY 178 EPGTGIGLAPLEF--VVVNRKASTADVYSPGILMAVAVLAGR-----E 219
 DB 359 QV-STRRYMAPVLEGLINFGDAPFLRIDVTKMGLVME-LASRCTAADGPVDEYMLPPE 416
 QY 220 VELTPESL--VTEAVCNQNRPSLAELPQACPERTPGLEGKELMOLCSSEPKDRPSFO 277
 DB 417 EELGQHSLEDMQEVVYVHKRRPVLDYWG--KHAGAMLCETIECDMDHAEARLS-A 472
 QY 278 ECLPKTDEVFQVVENNMNAVSTVDFLS 306
 DB 473 GCLGERITOMORLTN-----ITTEDIVT 496

RESULT 11
 AVR2_BOVIN STANDARD: PRT: 513 AA.
 AC Q28043;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
 GN ACTR2 OR ACTR1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCBI_TaxId=9113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOLSTEIN; TISSUE=Testis;
 RA MEDLINE=93203477; PubMed=7534730;
 RA Eshler J.F., Houde A., Lusier J.G., Silverstein D.W.;
 RT "Bovine activin receptor type II cDNA: cloning and tissue
 RT expression.";
 RL Mol. Cell. Endocrinol. 106:1-8(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA MEDLINE=97032546; PubMed=8675905;
 RA Montague L.V., Heriz A., Flavin N., Rogers M., Ennis S.,
 RA "Fluorescent in situ localization of the bovine activin receptor type
 RT IIA locus on chromosome 2 (2q3.3-2.4).";
 RL Mamm. Genome 7:869-869(1996).
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 TGBR RECEPTOR SUBFAMILY.

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 or send an email to license@sib.sib.ch).

DR EMBL: L21717; AAA74597.1; -
 DR EMBL: U43208; AAC48694.1; -
 DR HSSP: P27038; 18TE.
 DR InterPro: IPR000333; ActivinIL_receptor.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR Pfam: PF01064; Activin_recpt.1.
 DR Pfam: PF00069; Pkinase.1.
 DR PRINTS: PR00653; ACTIVINR.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Transmembrane; Glycoprotein; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 513
 FT DOMAIN 20 513
 FT TRANSMEM 136 161
 FT DOMAIN 162 513
 FT DOVAIN 192 485
 FT NP_BIND 198 206
 FT BINDING 219 219
 FT ACT_SITE 322 322
 FT CARBOHYD 43 43
 FT CARBOHYD 66 66
 SO SEQUENCE 513 AA: 57951 MW: C2969A54CF00617B CRC64;

Query Match 10.5%; Score 290.5; DB 1; Length 513;
 Best Local Similarity 29.5%; Pred. No. 6.5e-11;
 Matches 97; Conservative 57; Mismatches 126; Indels 49; Gaps 14;

12 PAPVLSIELENOELVGKDGFTVRAQHRKGVDAVKIV-----NSKAIISREVKAMAS 66
 DB PSLPLGKLPQLLEVKARGRFCGVMAQ--LLNEVAVAKIPIPDQKSMQNEVEVYSLPG 240
 QY 183 PSLPLGKLPQLLEVKARGRFCGVMAQ--LLNEVAVAKIPIPDQKSMQNEVEVYSLPG 240
 QY 67 LDNEVFLRLEGVIERVKNQDPRPALVTKFMENSGLSGLDSOCPRPPLCLRLKEVYL 126
 DB 241 MKHENILOFIGA-EKRGTSVDVDMLTITAFHEKGLSDPLKANYV-SMNEICHIATETMAR 298
 QY 127 GMFYLD-----ONPVLLHRDLKPSNVLPDEPLHVKLADFGLS-TFQGSQSGTSGS 177
 DB 299 GLAVLHEDIPGLKDGHRPAISHRDIKSKVLLKNNLFCIADFLALFKPAGKSGDTHG 358
 QY 178 EPGTGIGLAPLEF--VVVNRKASTADVYSPGILMAVAVLAGR-----E 219
 DB 359 QV-STRRYMAPVLEGLINFGDAPFLRIDVTKMGLVME-LASRCTAADGPVDEYMLPPE 416
 QY 220 VELTPESL--VTEAVCNQNRPSLAELPQACPERTPGLEGKELMOLCSSEPKDRPSFO 277
 DB 417 EELGQHSLEDMQEVVYVHKRRPVLDYWG--KHAGAMLCETIECDMDHAEARLS-A 472
 QY 278 ECLPKTDEVFQVVENNMNAVSTVDFLS 306
 DB 473 GCVGERITOMORLTN-----ITTEDIVT 496

RESULT 12
 AVR2_HUMAN STANDARD: PRT: 513 AA.
 ID AVR2_HUMAN
 AC P27037; Q92474;

01-AUG-1992 (rel. 23, Created)
 01-AUG-1992 (rel. 23, Last sequence update)
 16-OCT-2001 (rel. 40, Last annotation update)
 Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II) (ACTRIIA).
 ACVR2.
 Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA MEDLINE=92182002; PubMed=1311955;
 RA Matzuk M.W., Bradley A.;
 RT Cloning of the human activin receptor cDNA reveals high evolutionary
 RT conservation.;
 RL Biochim. Biophys. Acta 1130:105-108(1992).
 (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA MEDLINE=92231944; PubMed=1314589;
 RA Donaldson C.J., Mathews L.S., Vale W.W.;
 RT Molecular cloning and binding properties of the human type II
 RT activin receptor.;
 RL Biochem. Biophys. Res. Commun. 184:310-316(1992).
 (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Geisler A.G.;
 RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
 (4)
 RP SEQUENCE FROM N.A.
 RA Timmra T., Oida S.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGFB RECEPTOR SUBFAMILY.
 CC
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 CC
 CC EMBL; X63128; CAA44839.1; -
 CC EMBL; X62381; CAA44245.1; -
 CC EMBL; M93415; AAA5504.1; -
 CC EMBL; D31770; BAA06548.1; -
 CC PIR; S18908; S18908.
 CC PIR; J01486; J01486.
 CC PIR; S22345; S22345.
 CC HSP; P27038; IRYE.
 CC NIM; I02581; -
 CC InterPro; IPR000333; ActivinII_receptor.
 CC InterPro; IPR000472; Activin_rec.
 CC InterPro; IPR000719; Euk_kinase.
 CC InterPro; IPR002290; Ser_thr_kinase.
 CC Pfam; PF01064; Activin_rec; 1.
 CC Pfam; PF00069; Pkinase; 1.
 CC PRINTS; PR00553; ACTIVINR.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 19
 CC CHAIN 20 513
 CC DOMAIN 20 135
 CC EXTRACELLULAR (POTENTIAL).

TRANSMEM 135 161 POTENTIAL.
 DOMAIN 162 313 CYTOPLASMIC (POTENTIAL).
 DOMAIN 192 485 PROTEIN KINASE.
 NP_BIND 198 206 ATP (BY SIMILARITY).
 BINDING 219 219 ATP (BY SIMILARITY).
 ACT_SITE 322 322 BY SIMILARITY.
 CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CONFLICT 13 13 L->V (IN REF. 4).
 CONFLICT 204 206 GCV->PSL (IN REF. 4).
 CONFLICT 348 348 E->V (IN REF. 4).
 SEQUENCE 513 AA; 57847 MW; A89822E80979618 CRC64;
 SO
 Query Match 10.5%; Score 290.5; DB 1; Length 513;
 Best Local Similarity 29.5%; Pred. No. 6.5e-11;
 Matches 97; Conservative 57; Mismatches 126; Indels 49; Gaps 14;
 QY 12 PAPVLSIELEENELVGRDGTVAORRRKRGYDAVKIV-----NSRAISREYKAKAS 66
 DB 183 PSLPLGLKPLQLLEEVANARGRFCVWKAO--LLNETYAVKIFPIODQSDQNDNEYVYSLPG 240
 QY 67 LDNEFVRLRGVLEKVMQDPKPAVYTKFMENGLSGLLQSCPPRPPLCLRLKEVYL 126
 DB 241 MKHENILQFIQA-EKRGTSVDYDLMLITAFHEKGLSDFLKAVV-SMNELCRIAEYMAR 298
 QY 127 GMFYLD-----QNPVLLHRDLKPSNVLPDPELHVKLADFGLS-TEQGSQSGTSG 177
 DB 299 GLAYLHEDIPGLDGHKPAISHRDIKSNVLLKNNLPACIADGLAKFEAGKSGDTHG 358
 QY 178 EPGGTGLTYLPELF---VNVNRKASTASDYSGFLLMNVNLAGR-----E 219
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 QY 278 ECLPRTVEFQVNNNNNAAVSTVEDFLS 306
 DB 473 GCGVERITOMORLTN-----ITTEDIVT 496
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 ID AVR2_MOUSE PRT; 513 AA.
 AC P27038;
 DT 01-AUG-1992 (rel. 23, Created)
 DT 01-AUG-1992 (rel. 23, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
 DE ACVR2 OR ACVR2A.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91256317; PubMed=1646080;
 RA Mathews L.S., Vale W.W.;
 RT Expression cloning of an activin receptor, a predicted transmembrane
 RT serine kinase.;
 RL Cell 65:973-982(1991).
 (2)
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 25-121.
 RX MEDLINE=99101377; PubMed=9886286;
 RA Greenwald J., Fischer W.H., Vale W.W., Choe S.;
 RT Three-finger toxin fold for the extracellular ligand-binding domain
 RT of the type II activin receptor serine kinase.;
 RL Net. Struct. Biol. 6:18-22(1999).
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN, TESTIS, INTESTINE, LIVER, AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGF RECEPTOR SUBFAMILY.
 CC This SWISS-Prot entry is copyright: It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M65287; AAA37171.1; -
 DR PIR: A39896; A39896.
 DR PDB: 1BTE; 09-FEB-99.
 DR MGD: MGI:102806; Acvrt2.
 DR InterPro: IPR000333; ActivinII_receptor.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF01064; Activin_resp.1.
 DR Pfam: PF00069; Pkinase.1.
 DR PRINTS: PR00653; ACTV1N2R.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Receptor: Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 513
 FT DOMAIN 20 135
 FT TRANSMEM 136 161
 FT DOMAIN 162 513
 FT DOMAIN 192 485
 FT NP_BIND 198 206
 FT BINDING 219 219
 FT ACT_SITE 322 322
 FT CARBOHYD 43 43
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 QY 127 GNFYLDH-----ONVYLHRLDKPSNVLPDELPYTKADGSL-TOGGSGSTGSG 177
 DB 299 GLAYLHEDIPGLDKGHRKRAISHROKSNVYLKNNLACIADGGLKLEAKSGDTHG 358
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 QY 220 VELLPEPST--VYEAVCNRONRPSLAEPLQAGPETPGLLEKLMQLCWSSEPKRPSFQ 277
 DB 417 EEIGQPSLEDHQEVYVHKRRKRPVLRDYO---KHAGNMLCTIEECCHDAEARLS-A 472
 QY 278 ECLPKTDEVFOVVENNNMAAVSTVKDFLS 306
 DB 473 GCYGERITOMKRLTN-----IITTEDIVT 496
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M3K9_HUMAN
 ID M3K9_HUMAN STANDARD; PRT; 394 AA.
 AC P80192;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mitogen-activated protein kinase kinase kinase 9 (EC 2.7.1.1-) (Mixed
 DE lineage kinase 1) (Fragment).
 GN MAP3K9 OR MK1 OR PRKEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eultheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=colon epithelium;
 RX MEDLINE=93238756; PubMed=8477742;
 RA DOROV D.S., DEVEREUX L., DIETZSCH E., DE KRETSER T.;
 RT Identification of a new family of human epithelial protein kinases
 RT containing two leucine/isoleucine-zipper domains.";
 RL Eur. J. Biochem. 213:701-710(1993).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN EPITHELIAL TUMOR CELL LINES OF
 CC COLONIC, BREAST AND OESOPHAGEAL ORIGIN.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 CC PIR: S32467; S32467.
 DR PIR: J00229; J00229.
 DR HSP: P11362; 1PCK.
 DR MIM: 600136; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase.1.
 DR SMART: SM00219; TYRKC.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KM Transferrase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KM ATP-binding.
 FT NP_BIND 1 1
 FT DOMAIN 3 271
 FT NP_BIND 9 17
 FT BINDING 30 30
 FT ACT_SITE 127 127
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 QY 69 NEFYLRLEGYIEKVNNDODPKPALVYKEMENSLGSLQSCRRPPLCLRLLEKYL 128
 DB 59 HPNITLARGYCLK---EPNLCLYMERFARGCPLNRVLSKRIRP-DILVNNAVQIARAH 112
 QY 129 FYLIDQNFV-LIHRDLKPSNVLPDELPYTKADGSL-TOGGSGSTGSGEP 179
 DB 113 NYLDEAIVPIYIHRDKSSNLIILQNVENGDSLKIKITDFELAR-----EWHRTTKMSA 168
 QY 180 GGTIGYAPLPLFVAVNRK--STADSVYSGITLMAVLAQRVEYALPFE-----SLVYEA 233
 DB 169 AGTAMKAPF---VIRASNEKSGSDVSYGLMELLTG---EVFPRIQDLRAVATGYA 221
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 DB 222 MNKILAP---IPSTCEP-----FAKLMEDCMNPDPHSRPSFTNILDQLTIESGCFE 272

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284	spGluValIPheGlnMetValGluAsnAsnMetAsnAlaValaSerThr	300
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- Sequence 7, Application US/09531914
- Patent No. 6267956
- GENERAL INFORMATION:
- APPLICANT: ZENECA Limited
- TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
- FILE REFERENCE: PHM.70536
- CURRENT APPLICATION NUMBER: US/09/531,914
- CURRENT FILING DATE: 2000-03-21
- PRIOR APPLICATION NUMBER: 09/329,418
- PRIOR FILING DATE: 1999-06-11
- NUMBER OF SEQ ID NOS: 39
- SOFTWARE: FastSeq for Windows Version 3.0
- SEQ ID NO 2
- LENGTH: 1557
- TYPE: DNA
- ORGANISM: Homo Sapiens
- US-09-531-914-2

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34 hrvAlaPheArgAlaGlnIleAsnArgIlystrGlyTyrAspValAlaValLys 50
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51 lIleValAsnSerLysAlaAlaIleSerArgGluValLysAlaMetLalaSerLe 67
151 ATCGTAAACTCCAAAGCCCATATCCAGGAGAGCTCAAGGCCATGGCAATCTT 200
67 uaspasngluPheValLeuArgLeuGluGluGluValAlaIleGluLysValAsnT 84
201 GGTATACGAATTCGTGCTGCGCCCTACAAAGCGCTTTATCCGAGAGCTGAAC 250
84 rIpaSpGlnAspProLysProAlaLeuValThrLysPheMetGlnAsnGly 100
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: Sequence 1, Application us/09329418
: Patent No. 6096539
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/329,418
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 1873
: TYPE: DNA
: ORGANISM: Homo Sapiens
: US-09-329-418-1

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316  rIleProGIuSerGIyGIuGIyThrGIuMetAspGIyPheArgTr 333
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1115  TATCCAGAGTCCAGGCCAAGAGGAGCAAAATGATGGCTTTAGAGAA 1164
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333  hrIleGIuAsnGIuIaSerArgAsnAspValIeMetValSerGIuTrIleu 349
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350  AsnIyIeunIeunIeunGIuIuProProSerSerValProIyIyCysPr 366
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366  oSerLeuThrIyAspSerArgAlaGIuIuGIuIuValProGIuAlaI 383
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1315  GGACAGAGGACATCTTCAATGATGAGGCCCAACCTCCCAAGACCCA 1364
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1365  GAGACCTCACTTCAAGAAACAGATGCCAGCCCTCACTCACTGAGAC 1414
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416  rProSerProGIyProArgIyAsnGIuIuIaGIuIuArgIuGIyMetA 433
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1415  ACCAAGTCTCGAGCCCGAGAGGAAATCAGGGGCTGAGAGACACATGA 1464
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433  snTrpSerCysArgThrProGIuProAsnProValThrGIyArgProIe 449
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1515  GTTAAACATATCAACTGCTGTGGGTGCAAGTTGGAGACAACTACTT 1564
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   |||||||
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   |||||||
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seq_documentation_block:
; Sequence 1, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531.914
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1073
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-531-914-1

alignment_scores:
Quality: 2714.50      Length: 519
Ratio: 5.271          Gaps: 1
Percent Similarity: 99.229  Percent Identity: 98.651

alignment_block:
US-09-762-491-6 x US-09-531-914-1 ..

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Align seg 1/1 to: US-09-531-914-1 from: 1 to: 1873

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17 TlEgIuSgIuSgInGInGInIuEValGlyIySAspGlyPheGlyT 34
  |||
215 CATGAGAACTGGAGAACAGAGAGCTCGCGCAAGCGGGTTCGCA 264
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34 hVAlPheAArgAlaGInHIsArgIyTrGlyIyTrAspValAlaValIyS 50
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265 CAGTGTCTCGGCGCAACATAGAGAGTGGGCTACGATGCGCGTCAAG 314
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51 TlEValAsnSerIySAlaIleSerArgIyValIySAlaMetAlaSerIe 67
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67 uASpAsnGluPheValLeuArgLeuGluIyValTlEgIuIySValAsnT 84
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100 GlySerLeuSerGIyLeuLeuGInSerGInCySProArgProTProIe 116
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116 uLeuCyArgLeuLeuIySgIuValIyLeuGlyMeCherIyLeuHIsA 133
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266 pSerSerGIyProIySAspArgProSerPheGInIySLeuProIyArg 283
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seq_name: /cgn2_6/ptodata/2/lna/5/_CONB.seq:us-08-444-005-14
seq_documentation_block:
; Sequence 14, Application US/08444005
; Patent No. 5674734
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Seed, Brian
; APPLICANT: Stanger, Ben L.
; APPLICANT: Lee, Tae-Ho
; APPLICANT: Kim, Emily
; TITLE OF INVENTION: CELL DEATH PROTEIN
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.

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STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,005
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00383/026001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-444-005-14

alignment_scores:

Quality: 445.50 Length: 603
Ratio: 1.442 Gaps: 23
Percent Similarity: 51.244 Percent Identity: 26.202

alignment_block:

US-09-762-491-6 x US-08-444-005-14 ..

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31 yheGlyThrValPheArgIleGlnIleArgIleArgIleValAla 48
132 CTTCGGGAAGGTCTCTGTGTACACAGAAAGCATGATGTCTATCC 181
48 IValIleValIleAsn.....SerIleAlaIle 57
182 TGAAGAAAGATACACAGAGCCCAACCCGCTGATACATGACGTCTC 231
58 SerArgGluValIleValIleMetAlaSerIleAsnArgIlePheValAla 74
232 TTGGAAAGGGGAGAGATGATGACAGACTGAGACACACTCGAGGTGAA 281
74 GLeuGluGly...ValIleGluValIleAsnTrpAspGlnAspProLys 90
282 GCTACCTGGCATCATCATAGAGAAAGGCACTAT..... 315
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316 ..TCGGAGGATGAGTACATGAGAAAGGAGAACCTGATCCACCTCTCA 363
107 GlnSerGlnCysPheArgProTrpProIleLueLueCysArgLeuLeu 123
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140 IAsArgAspLeuLysProSerAsnValLeuProAspProGluLeuIleVal 156
458 ACAAGACCTGAAACCTGAGAAATATCTCTGTGATCGTACCTTTCATT 507
157 LysIleValIleAspPheGlyLueSerThrPheGlnGlySerGln..... 171
508 AAGATAGCCGATCTGTGTGCTTCTTAAAGCATGAGCAAACTGAC 557
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558 TAAGAGAAAGACAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
178 IupProGlyThrIleGlyThrLeuAlaProGluLeuPheValIleVal 194
608 ACAATGCTGTACCTTACTACATGACACCCGAAACCTGAATGACATC 657
195 AsnArgLysAlaSerThrLysSerAspValTyrSerPheGlyIleLeu 211
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832ATCATCGCTCATGACAGCGCTGCTGCAGCCATCC 868
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: Sequence 257, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Murist, Rene
: APPLICANT: Muriel, James Greg
: TITLE OF INVENTION: Compositions and Methods for Their Use
: FILE REFERENCE: 11000, 1011c1
: CURRENT APPLICATION NUMBER: US/09/188,930A
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FASTED for Windows Version 3.0
: SEQ ID NO: 257
: LENGTH: 3516
: TYPE: DNA
: ORGANISM: Mouse
: US-09-188-930-257

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Quality: 424.50 Length: 594

Ratio: 1.415 Gaps: 26

Percent Similarity: 50.505 Percent Identity: 27.441

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US-09-762-491-6 x US-09-188-930-257 ..

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62 LyAlaMetAlaSerLeuAspAsnGluPheValLeuArgLeuGlyVal 78
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344	evaISeerGluTrpLeuAsnLyLeuAsn.....Leu	354
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1630	ATGCATGTGAAGCTGCCAGCATGACAGAGAAATGTGTGGCCACCTGCT	1679
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seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:05-09-132-118-1

seq_documentation_block:

Patent No. 6211337

APPLICANT: BAICHW

APPLICANT: HSU, HAILING

TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN

NAME OF INVENTOR:	ADDRESS:
TITLE OF INVENTION:	ASSAYS

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & IE
STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH
STATE: CALIFORNIA

COUNTRY: USA
ZIP: 94010

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY

OPERATING SYSTEM: PC-DOS/MS

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: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CTBPRENT APPLICATION DATA:
:

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APPLICATION NUMBER: US/09/132,118

CLASSIFICATION
ATTORNEY / AGENT

NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 75

REFERENCE/DOCKET NUMBER: T95-006-1

TELEPHONE: (650) 343-4341

INFORMATION FOR SEQ ID NO: 1:

LENGTH: 2016 base pairs

STRANDEDNESS: double

MOLECULE TYPE: CDNA

NAME/KEY: CDS

DOCUMENT: 11-2013
US-09-1332-118-1

Alignment_Score: 423

Ratio:	1.4
Percent StimJartty:	50.

Attachment block:

US-09-102-491-6 X US-09-

Align seg 1/1 CO: US-09

1/ Settle up the balance

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33 yth rValpneargAla ...

87 GAAGCTGTCCTCTGTGT

45TyrAspValAla

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; Documentation_block:
; Sequence 1, Application US/09132118
; Patent No. 611137
; GENERAL INFORMATION:
; APPLICANT: BAICHWAL, VIJAY R
; APPLICANT: HUANG, JIANNING
; APPLICANT: HSU, HAILING
; APPLICANT: GOEDEL, DAVID V
; TITLE OF INVENTION: RIP NOVEL HUMAN PROTEIN INVOLVED IN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
; TYPE OF INVENTION: ASSAYS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/132,118
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: 795-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2013
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; Quality: 423.00 Length: 580
; Ratio: 1.434 Gaps: 23
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seq_documentation_block:

Sequence 16, Application US/08444005

Patent No. 5674734

GENERAL INFORMATION:

APPLICANT: Leder, Philip

APPLICANT: Seed, Brian

APPLICANT: Stanger, Ben Z.

APPLICANT: Lee, Tae-Ho

APPLICANT: Kim, Emily

TITLE OF INVENTION: CELL DEATH PROTEIN

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/444,005
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,164
 REFERENCE/DOCKET NUMBER: 00383/026001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2137 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-444-005-16

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# Patent No. 6020198
# GENERAL INFORMATION:
# APPLICANT: C. Frank Bennett
# TITLE OF INVENTION: Lex M. Cowsett
# FILE REFERENCE: RTS-0011
# CURRENT APPLICATION NUMBER: US/09/161,443A
# NUMBER OF SEQ ID NOS: 47
# SEQ ID NO 1
# LENGTH: 2617
# TYPE: DNA
# ORGANISM: Homo sapiens
# FEATURE:
# NAME/KEY: CDS
# LOCATION: (1)..(2016)
# FEATURE:
# NAME/KEY: unsure
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# OTHER INFORMATION: unknown
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# NAME/KEY: unsure
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273 rGProSerPheGlnGluCysLeuProlyThrAspGluValPheGln... 288
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316 .....SerLeProGluSer..... 320
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1012 GAACAGCTGTCTCACTGACACTCCAGAGACTGTGGATGGTCTCTGT 1061
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342 SP.....Val.Me 344
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356 .....GluProProSerSerVal 361
1212 TTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261
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1262 CACAGCAA.....GACCTTACGAGAAATTTTCAGAAATTCAGAGGAGAA 1305
378 nVal.....P 380
1306 GGCAGCTGTATTTCAGTGCAGCCAGTCTATTCAGTGCAGCAGCC 1355
380 rGlnAlaLeuTrpThrAla..... 385
1356 CTCAGGGGCTACAGCCAACTCAAGTACTGTATCAGAAACAATGATAT 1405
386 .....GlyThrSerSerAspSerMetAlaGlnProProGlnTh 398
1406 ATAGCTCACATGCGCTTTCAGACAGACAGTGCATGCAGAAACAGGT 1455
398 rProGluThrSerThrPheArgAsnGlnMetProSerProThrSerThr 415
1456 CCCAGAGTTTGTATCAGG.....CCAATTCAGAGTC 1486
415 LysThrProSer.....ProGlyProArgGlyAsnGlnGlyAla 427
1487 ATATGCGTATGTCATATATATCCAGTGGCTGAGACCAATATATATGCA 1536
428 GluArgGlnGlyMetAsnTrpSerCysArgThrProGluProAsnProVa 444
1537 AATATACCCAGCATTCATTCAGTCTTCCACCCACAGATGAATATAT 1586
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seq_documentation_block:
/ Sequence 2, Application US/09133944
/ Patent No. 6280937
/ GENERAL INFORMATION:
/ APPLICANT: Luo, Ting
/ APPLICANT: Luo, Pei Wen
/ TITLE OF INVENTION: SHUTTLE VECTORS
/ FILE REFERENCE: A66252/DJB/DAY
/ CURRENT APPLICATION NUMBER: US/09/133,944
/ EARLIER APPLICATION NUMBER: 09/133,949
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 9687
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: constructed
US-09-133-944-2

alignment_scores:
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Ratio: 1.357 Gaps: 23
Percent Similarity: 50.862 Percent Identity: 25.862
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1170 TCCAGTACTTCTCTGGAGAGTGCAGAACTG...GACACGGAGGCTTGG 1216
33 yThrValPheArgAlaGlnHisArgLysTrpGly..... 44
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45 ....TyraPvalAlaValLysIleValAsnSerLysAlaIleSerArg 59
1267 CAGTGTACAGAGGCGCCCACTGCTTGAACACACAGAGCCCTTGGAG 1316
60 GluValLysValMetAlaSerIleuAspAsnGluPheValLeuArgLeuCl 76
1317 GAGGCGAAAGATGATGAACAGACTGAGACACAGCCGGGTGTGAAGCTCT 1366
76 uGlyValIleGluLysValAsnTrpAspGlnAspProLysProAlaLeu 93
1367 GGCCTCATC.....ATAGAGGAGAGGAGAACTCTCTG 1401
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160 AspPheGlyLeuSerThrPheGlnGlySerGln..... 171
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172 .....SerGlyThrGlySerGlyGluProGlyG 181
1645 GCACAAATAGCTGAGCGAAGTGCAGCGACCGCTAAG...AAGAAATGGCG 1691
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198 AlaSerThrAlaSerAspValTyrSerPheGlyIleLeuMetTrpAlaVal 214
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231 lValAlaValCysAsnArgGln.....AsnArg 239
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1818 ATGCTATGTGTGACAGCAGAGTGTGATTAATGCAATAAATCTGGGAAGG 1867
240 ProSerLeuAlaGluLeuProGlnAlaGlyProGluThrProGlyLeuGlu 256
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256 uGlyLeuLysGluLeuMetGlnLeuLysTyrPheSerSerGluProLysAsp 273
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1907 ....ATTATCAGTCTCATGAAAGCTGTGTGGAGCAAGAAATCCGAGATC 1992
273 rProSerPheGlnGluCysLeuProLysThrAspGluValPheGln... 288
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2141 GAACAGCCTGCTCATCTGCAAGTTCACAGCGACTTGGAGTGGCGCTGT 2190
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342 sp.....Val 344
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seq_documentation_block:
; Sequence 2, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiko
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: US-03133
; CURRENT APPLICATION NUMBER: US/09/069, 023A
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-069-023-2

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Ratio: 1.951 Gaps: 11
Percent Similarity: 63.077 Percent Identity: 32.308

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118  sArGLeuLeuLySGluValValLeuGlyYmeRPheryfLeuHisAspGlna 135
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168  ...GIYGlySerGlnSerGIYThcGISerGlyVgluPro...GIYGIYT 182
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293  AsnMetAlaenAlaAlaValSerThrValALysaSPheLeuSerClnLeuY 309
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# Sequence 2, Application US/09019942
# Patent No. 6033855
# GENERAL INFORMATION:
# APPLICANT: Berlin, John
# TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
# NUMBER OF SEQUENCES: 4
# CORRESPONDENCE ADDRESS:
# ADDRESSEE: Fish & Richardson P.C.
# STREET: 225 Franklin Street
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Dikette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTEST for Windows Version 2.0b
APPLICATION NUMBER: 05/09/019,942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Melilejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
OS-09-019-942-2

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168 ...GlyGlySerGlnSerGlyThrGlySerGlyLeuPro...GlyGlyT 182
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seq_documentation_block:
: Sequence 1, Application US/0909041A
: Patent No. 6340576
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
: FILE REFERENCE: 07334-076001
: CURRENT FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 09/019,942
: NUMBER OF SBO ID NOS: 37
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SBO ID NO 1
: LENGTH: 1931
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (214)...(1833)

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    Percent Similarity: 62.696      Percent Identity: 31.661

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294 CGCCTCTGGGCACTGTGTCTGCCGCCGCGCAGCAGACTGGCGCTCCAG 343
47 AlAlaValLysLleValAsn.....Ser 54
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55 LysAlaLleSerArgGluValLysAlaMetAlaserLeuAspAsnGluP 71
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Date: Aug 13, 2002 11:21 PM

About: Results were produced by the GenCore software, version 4.5.

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Search information block:

Query: US-09-762-491-6
Query length: 519
Database: N.Geneseq.032802.*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 201.680000

score_list:

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seq_documentation_block:

ID AA50788 standard; DNA; 1557 BP.

AA50788:

31-MAY-2000 (first entry)

Human Apop3 DNA.

Apop3 protein; apoptotic protein; apoptosis modulation; immunotherapy;
apoptosis-mediated disorder; cancer; autoimmune disorder; cytostatic;
degenerative disorder; viral infection; cell loss;
inhibitor of apoptosis protein; IAP; ss.

Homo sapiens.

Key 1.1557 Location/Qualifiers
CDS /tag= "Apop3 protein"
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MO200007545-A2.

17-FEB-2000.

06-APR-1999; 99WO-US17776.

06-APR-1998; 98US-0095587.

06-APR-1998; 98US-0095590.

08-SEP-1998; 98US-0099486.

(RIGF-) RIGEL PHARM INC.

Luo Y, Huang BCB, Shen M, Yu PW;

WPI: 2000-20547/18.

P-PSDB: AAY45042.

Novel apoptotic proteins Apop1, Apop2 and Apop3 and recombinant nucleic acids encoding them for use in screening modulators which is useful for diagnosis and treatment of diseases

Claim 2; Fig 5; 64pp; English.

The patent discloses the use of novel apoptotic proteins and related molecules involved in apoptosis modulation. Expression vectors comprising the Apop DNA can be used to transform host cells. Apop DNA can be administered as DNA vaccines. Apop proteins are used to make polyclonal and monoclonal antibodies for use in immunotherapy. The proteins are useful in treating apoptosis-mediated disorders including cancer, autoimmune disorders, sustained viral infection, inappropriate cell loss and degenerative disorders. Drug candidates that affect Apop bioactivity are identified by screening. The present sequence encodes Apop3 protein. This was identified using RFP (receptor-interacting protein) as the bait protein employing the yeast two-hybrid screening system. Human Apop3 is expressed in heart, liver, pancreas, placenta, and lung. Overexpression of Apop3 inhibits TNF (tumour necrosis factor) alpha-induced caspase activation without affecting TNFalpha-induced NFkappa B activation.

Sequence 1557 BP; 397 A; 424 C; 446 G; 290 T; 0 other:

alignment_scores:

Quality: 2770.00 Length: 518
 Ratio: 5.347 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

Alignment block:
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Align seg 1/1 to: AA50788 from: 1 to: 1557

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 XX
 AC AAA47702:
 XX
 DT 08-NOV-2000 (first entry)
 XX

DE Kinase of death (KOD) CDS.
XX KOD: kinase of death; programmed cell death; apoptosis; cancer;
KW autoimmune disease; stroke; Alzheimer's disease; identification; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1557
XX /tag- a
XX /product- Kinase of death
XX
XX US6096539-A.
XX
XX 01-AUG-2000.
XX
XX 10-JUN-1999; 99US-0329418.
XX
XX 10-JUN-1999; 99US-0329418.
XX
XX (ZENE) ZENECA LTD.
XX
XX Gomes BC, Prosser JC, Kasof GM;
XX WPI: 2000-523872/47.
XX DR P-PSDB; AAB01534.
XX
XX New nucleic acids encoding a protein activator of apoptosis for
XX PT preventing, diagnosing and treating pathophysiological disorders
XX related to apoptosis
XX
XX Claim 3; Columns 31-32; 32pp; English.
XX
XX The kinase of death (KOD) polypeptide is integral to the activation
XX process of cellular apoptosis (programmed cell death). Apoptosis is
XX needed to orchestrate biological maintenance of an organism during
XX development as well as to preserve the normal function and fitness of
XX tissues during a normal life span. Physiological conditions which
XX result from aberrant apoptosis may be dire. Cancer and autoimmune
XX disease may result when there is too little apoptosis as well as
XX severe stroke damage or the neurodegeneration of Alzheimer's disease
XX when there is too much apoptosis. The KOD polypeptide is useful for
XX studying pathophysiological disorders related to apoptosis as well
XX as for identifying compounds that modulate biological and/or
XX pharmacological activity of the native mediator of apoptosis.
XX
XX Sequence 1557 BP; 395 A; 422 C; 448 G; 291 T; 1 other:

alignment_scores:

Quality: 2744.00 Length: 518
Ratio: 5.328 Gaps: 0
Percent Similarity: 99.421 Percent Identity: 99.228

alignment_block:

US-09-762-491-6 x AAA47702 ..

Align seg 1/1 to: AAA47702 from: 1 to: 1557

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AC AAK94599;
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DF 06-NOV-2001 (first entry)
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DE Human full-length cDNA, SEQ ID NO: 3541.
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KW Human: full length cDNA; cDNA synthesis: oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
XX
PR 11-JAN-2000; 2000JP-0118774.
XX
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
PI WPI: 2001-524255/58.
XX
DR P-PSDB; AAK93664.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
XX
PT use in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 3541: 1380bp + sequence listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
XX
CC clones. 830 cDNA molecules encoding a human protein have been
XX
CC isolated and nucleotide sequences of 5'- and 3'- ends of the cDNA
XX
CC molecules have been determined. Primers for synthesizing the full length
XX
CC cDNA are useful for clarifying the function of the protein encoded by
XX
CC the cDNA. The full length clones were obtained by construction of full
XX
CC length enriched cDNA libraries that were synthesised by the oligo-capping
XX
CC method. The primers enable the production of the full length cDNA easily
XX
CC without any special methods. The present sequence is a full length
XX
CC human cDNA of the invention.
XX
CC Note: The sequence data for this patent did not form part of the printed
XX
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
XX
Sequence 1871 BP; 474 A: 528 C: 516 G: 353 T: 0 other:

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alignment_scores:

Quality: 2737.00 Length: 519
 Ratio: 5.304 Gaps: 1
 Percent Similarity: 99.422 Percent Identity: 99.229

alignment_block:

US-09-762-491-6 x MAK94599 ..

Align seg 1/1 to: MAK94599 from: 1 to: 1871

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1 MetSerCyValLysLeuTrpProSerGlyAlaProAlaProLeuValSe 17
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165 ATGTCTGGCTCAAGTTATGCCCCAGCCAGGCTGCCGCCCTGGTGTG 214
17 TTTGGTGGTGGGCGCAACATAGGAAGTGGGCTACGATGTGGCGGTCA 264
215 CATCGAGAACTGGAGAACAGACGCTCTCGCCAAAGCGGCTCCGCA 264
34 hValPheArGAlaGlnHLeArGlyTrpGlyTyTrAspValAlaValLys 50
  |||||
265 CAGTGTCCGGGGCGCAACATAGGAAGTGGGCTACGATGTGGCGGTCA 314
51 TLeValAsnSerLysAlaIleSerArgGlyValLysAlaMetAlaSerLe 67
  |||||
315 ATGTTAACTCGAAGCGCATTCAGGAGGTCAGAGCCATGCGCAAGTCT 364
67 UAAPAsnGluPheValLeuArgLeuGluGlyValTLeGluLysValAsn 84
  |||||
365 GGTATACGAATTCCTCTCGCCCTAGAAAGGGGTATCGAAGAGTGAAC 414
84 rPheGlnAspProLysProAlaLeuValThrLysPheMetGluAsnGly 100
  |||||
415 GGAACCAAGATCCCAAGCCGGCTCTGGTACTTAATTAATGAGAACGGC 464
101 SerLeuSerGlyLeuLeuGlnSerGlnCySerProArgProTrpProLeu 117
  |||||
465 TCTGTGTGGGGTCTGTGAGTCCAGTCCCTGGCCCTGGCCGCTCT 514
117 uCyArGLeuLeuValValLysGlyMetPheTrpLeuHIsAsp 134
  |||||
515 TTCCCTCCCTCTAAAGAGTGGTCTGGCATGTTTACCTCGACGAGCC 564
134 LAsnProValLeuLeuHIsArgAspLeuLysProSerAsnValLeuPro 150
  |||||
565 AGAACCCGGTCTCTCGACCCGCACTCAAGCCATCCAAAGCTCTCTCG 614
151 AspProGluLeuHIsValLysLeuAlaAspPheGlyLeuSerThrPheG 167
  |||||
615 GACCCAGAGCTGCACGTCMAAGCTGGCAGATTGGCTGTCACATTTCA 664
167 nGlyGlySerGlnSerGlyThrGlySerGlyGluProGlyLysThrLeu 184
  |||||
665 GGGAGGCTCAAGTCAAGGACAGGCTCCGGGACCCAGGGGGGCACTGC 714
184 LysTrpLeuAlaProGluLeuPheValAsnValAsnArgLysAlaSerThr 200
  |||||
715 GACTACTGGCCCCAGAACTGTTGTAAGCTAAACCGGAAGCCCTCCAC 764
201 AlaSerAspValLysSerPheGlyLLeuMetTrpAlaValLeuAlaG 217
  |||||
765 GCCAGTACGCTCAAGCTTCGGGATCTTAATGGGGAAGCTGTGGTGG 814
217 YArgGluValGluLeuProThrGluProSerLeuValTrpGluAlaValC 234
  |||||
815 AAGAGAGTGAAGTTCACCAACGGAACATCACTGTCAGCAAGCAAGTGT 864
234 YAsnArgGlnAsnArgProSerLeuAlaGluLeuProGlnAlaGlyPro 250
  |||||
865 GCACAGAGCGAAGACGGCTTCATGCTGAGCTGCCCAAGCGGGGCT 914
251 GLeuThrProGlyLeuGluGlyLeuLysGlyLeuMetGlnLeuYsTrpSe 267
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915 GAGACTCCGGGCTTAGAAGAGACTGAAGAGCTTAATGAGCTGTGGTGG 964

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267 tSerGluProLysAspArgProSerPheGlnGluCysLeuProLysThrA 284
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284 sPGLuValPheGlnMetValGluAsnAsnMetAlaAlaValSerThr 300
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1015 ATGAAGCTTCCAGATGTGTGGAAGCAATATGAATGGCTGTGCTCCAG 1064
301 ValLysAspPheLeuSerGlnLeuLysSerAsnArgTrpPheSerL 317
  |||||
1065 GTAAAGATTTCTGTCTACGCTCAGGACCAATAGAGATTTCTAT 1114
317 eProGluSerGlyGlnGlyLysThrGluMetAspGlyPheArgTrpL 334
  |||||
1115 CCCAGAGTCAAGCCCAAGAGGACAGAAATGAGTGGCTTAGAGAGAAC 1164
334 LeGluAsnGlnHIsSerArgAsnAspValMetValSerGluTrpLeuAs 350
  |||||
1165 TAGAAACCAAGCACTCTCGTAATGATGTCAATGTTCTGAGTGGCTAAC 1214
351 LysLeuAsnLeuGluGluProProSerSerValProLysLysCySer 367
  |||||
1215 AAACGAAATTCAGAGAGCTCCAGCTCTGTCTTAAAAAATGCCGA 1264
367 eTrLeuThrLysArgSerArgAlaGlnGluGluValProGlnAlaTrp 383
  |||||
1265 GCCTTACCAAGAGAGAGGCGCAAGAGAGAGAGTCCCAAGCCCTGG 1314
384 ThrAlaGlyThrSerAspSerMetAlaGlnProProGlnThrProG 400
  |||||
1315 ACAGCAGGACATCTTAAGATGATGGCCCAAGCTCCCAAGCTCCAGA 1364
400 uThrSerThrPheArgAsnGlnMetProSerProThrSerThrGlyTrp 417
  |||||
1365 GACCTCAACTTTCAGAAACAGATGCCCAAGCTCAACTGGAACAC 1414
417 rSerProGlyProArgGlyAsnGlnGlyAlaGluArgGlnLysMetAs 433
  |||||
1415 CAAGCTCGAGCCCGGAGGAATCAGGGGGCTGAGAGCAAGCATGAAC 1464
434 TrpSerCyArGThrProGluProAsnProValThrGlyLysProLeu 450
  |||||
1465 TGGTCTCGAGACCCCGAGCCCAATCCAGTACAGGCGGACCCGCTCG 1514
450 LAsnLeuTrpAsnCysSerGlyValGlnValGlyAspAsnAsnTrpLeu 467
  |||||
1515 TAACTATTAACAACCTGCTGGGGTCAAGTTGGAGACAAACACTACTGA 1564
467 hMetGlnGlnThrThrAlaLeuProThrTrpGlyLeuAlaProSerGly 483
  |||||
1565 CTATCCAAACACAACTGCTTGGCCACATGGGCTTGGACCTTGGGGC 1614
484 LysGlyArgGlyLeuGlnHIsAspProProValGlySerGlnGluLys 500
  |||||
1615 AAGGGAGGGGCTTGCAGACACCCCACTAGATGTTCCGCAAGAACGCC 1664
500 oLysAspProGluAlaTrpSerArgProGlnGlyTrpLysHIsSerG 517
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517 LysLys 518
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1715 GGAAG 1719

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seq_name: /SIDSI/gcdata/hold-geneseg/geneseq -emb1/NA2000.DAT: AAA75675

seq_documentation_block:

ID AAA75675 standard; DNA; 2140 BP.

XX AAA75675;

AC

XX

DT 22-JAN-2001 (first entry)

DNA encoding a human regulator of intracellular phosphorylation.

Human: Intracellular phosphorylation regulator; HRP; stroke; myeloma;
neurological disorder; Parkinson's disease; demyelinating disease;
meningitis; developmental disorder; neuromuscular disorder; cancer;
myasthenia gravis; cell proliferative disorder; acinic keratosis;
arteriosclerosis; achroscleorosis; leukaemia; melanoma; bronchitis;
autoimmune disorder; inflammatory disorder; Addison's disease;
acquired immunodeficiency disease; allergy; diabetes mellitus;
rheumatoid arthritis; microbial infection; trauma; ss.

XO
XS Homo sapiens.
XX
XT Key Location/Qualifiers
FT /tag= "a
FT CDS /product= "regulator of intracellular phosphorylation"
FN NO2000S533Z-A2.
PN
PD
PE 21-SEP-2000.
PF 17-MAR-2000; 2000MO-US07277.
PR 18-MAR-1999; 99US-0125563.
PR 20-MAY-1999; 99US-0155009.
PR 09-JUL-1999; 99US-0133188.
PA (INCY-) INCYTE PHARM INC.
PI Bandman O., Tang YT., Yue H., Hillman JL., Baughn MR., Azimzal Y.;
PI Lu DM., Au-Young J;
PX XN WPI : 2000-602121/57.
DR P-PDB; AAB1658.
XX
PT Novel human intracellular phosphorylation regulator polypeptides and
polypeptides for diagnosis, prevention and treatment of
PT neurological , cell proliferative and autoimmune/inflammatory disorders

-

XU Claim 4: Page 88-89; 96pp: English.

The present sequence encodes a human regulator of Intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP polypeptide. HRIP and its agonist or antagonist are useful for treating a disease or condition associated with decreased or increased expression of functional HRIP. Diseases treated or diagnosed include [neurological] disorders such as stroke, Parkinson' disease, demyelinating diseases, bacterial and viral meningitis and other developmental disorders of the central nervous system, neuromuscular disorders, myasthenia gravis, cell proliferative disorders such as acicinic keratosis, arteriosclerosis, athroscleriosis and cancer including leukemia, melanoma, myeloma and cancer of the adrenal gland bladder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/inflammatory disorder such as Addison's disease, acquired immunodeficiency diseases, allergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial infection and trauma.

Sequence 2140 BP: 534 A: 610 C: 508 G: 408 T: 0 other:

Alignment_scores:
Quality: 2718.00 Length: 562
Ratio: 5.267 Gaps: 1
Percent Similarity: 91.815 Percent Identity: 91.637

Alignment_block:
US-09-762-491-6 x AAA75675 ..

Align seg 1/1 to: AAA75675 From: 1 to: 2140

[illegible]


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1064 GGAATGAGAGAGCTAATGAGCTCTGCTGAGACAGTGAAGCCAAAGGACAG 1113
273 GProserPhgIngluGluCysLeuProLysThrAspGluValPheGlnMetV 290
1114 ACCCTCTTCCAGAAATGCTTACCAAAAATCTATGACTCTTCCGATGC 1163
290 aIGuanAnanMetAnalaValSerThValLysAspPheLeuSer 306
1164 TGGAGAAATATGAAATGCTGCTCTCCAGCGTAAAGATTTCTCTGCT 1213
307 GlnLeuLysSerSerAnatArgPheSerIleProGluSerGlyGlnG 323
1214 CAGCTCAGAGAGACAAATAGACATTTCTATCCAGATCCAGCCAAAG 1263
323 YGlyThrGluMetAspGlyPheArgThrIleGluGlnMetLysSer 340
1264 AGGACACAAATGATGCTTGTGGAGAACATAGAAACAGAGCTCTC 1313
340 rGAsnAspValMetValSerGluTrpLeuAsnLysLeuAsnGluGlu 356
1314 GTAATGATGTCATGTTCTGAGCTGCTAAACAACTGAATCTGAGAGAG 1363
357 ProProSerSerValProLysLysCysProSerLeuThrLysArgSer 373
1364 CCTCCAGCTCTGCTCTTAAATAATCCGAGCCTTACCAAGAGAGAGAG 1413
373 gAlaGlnGluGluGlnValProGlnAlaTrpThrAlaGlyThrSer 390
1414 GGCCAAAGAGAGAGAGTTCACAAAGCTGGAGAGAGAGAGATCTTCAG 1463
390 sPSeMetAlaGlnProProGlnThrProGlnThrSerThrPheArgAsn 406
1464 ATTCAGAGGCCCCAACTCCCAAGACTCCAGACACTCAACTTTCGAAAC 1513
407 GluMetProSerProThrSerThrGlyThrProSerProGlyProArg 423
1514 CAGATGCCAGCCCTTACTCTCACTGAGAACCCAGCTCTGGACCCGAGG 1563
423 yAsnGlnGlyAlaGluArgGlnGlyMetAsnTrpSerCysArgThrPro 440
1564 GAATCAGGCGGCTGAGAGACAAAGGCAATGAACTGATCGAGAGAGAG 1613
440 LuProAnProValThrGlyArgProLeuValAsnIleTrpAsnCysSer 456
1614 AGCCAAATCCAGTACAGGCGGAGCGCTCTGTTACATATACAGCTGCT 1663
457 GlyValGlnValGlyAspAsnAsnTrpLeuThrMetGlnGlnThrAl 473
1664 GGGGTGCAAGTGTGAGACAACTACTGACTATGCAACAGACAACTGC 1713
473 aLeuProThrTrpGlyLeuAlaProSerGlyArgGlyArgGlnGln 490
1714 CTGGCCACATGGGGCTTGACCTTCGGGCAAGGGGAGGGGCTTGACG 1763
490 lAsProProProValGlySerGlnGluGlyProLysAspProGluAla 506
1764 ACCCCCAACAGTACGTTGCGCAAGAAAGCCCTTAAGAGTCTCGAAGCT 1813
507 SerArgProGlnGlyTrpTrpAsnHisSerGlyLys 518
1814 AGCAGGCGCACAGGTTGTAATCATATAGCGGGA 1849
seq_name: /SIDSI/gcysdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA47701
seq_documentation_block:
ID AAA47701 standard; cDNA; 1873 bp.
XX
XX AAA47701:
XX
XX 08-NOV-2000 (first entry)
XX
XX Kinase of death (KOD) coding sequence.
DE

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XX
XX KOD: Kinase of death; programmed cell death; apoptosis; cancer;
XX autoimmune disease; stroke; Alzheimer's disease; identification; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 165..1724
XX FT /*tag= a
XX FT /product= Kinase of death
XX
XX US6096539-A.
XX
XX 01-AUG-2000.
XX
XX 10-JUN-1999; 99US-0329418.
XX
XX 10-JUN-1999; 99US-0329418.
XX
XX (ZENEC) ZENEC LTD.
XX
XX Gomes BC, Prosser JC, Kasof GM;
XX
XX DR WPI: 2000-523872/47.
XX
XX P-PSDB: AAB01524.
XX
XX PT New nucleic acids encoding a protein activator of apoptosis for
XX PT preventing, diagnosing and treating pathophysiological disorders
XX PT related to apoptosis
XX
XX PS Claim 9: Columns 29-32; 32pp: English.
XX
XX CC The kinase of death (KOD) polypeptide is integral to the activation
XX CC process of cellular apoptosis (programmed cell death). Apoptosis is
XX CC needed to orchestrate biological maintenance of an organism during
XX CC development as well as to preserve the normal function and fitness of
XX CC tissues during a normal life span. Physiological conditions which
XX CC result from aberrant apoptosis may be dire. Cancer and autoimmune
XX CC disease may result when there is too little apoptosis as well as
XX CC severe stroke damage or the neurodegeneration of Alzheimer's disease
XX CC when there is too much apoptosis. The KOD polypeptide is useful for
XX CC studying pathophysiological disorders related to apoptosis as well
XX CC as for identifying compounds that modulate biological and/or
XX CC pharmacological activity of the native mediator of apoptosis.
XX
XX Sequence 1873 bp; 471 A; 531 C; 518 G; 353 T; 0 other:
XX
XX
XX alignment_scores:
XX Quality: 2714.50 Length: 519
XX Ratio: 5.271 Gaps: 1
XX Percent Similarity: 99.229 Percent Identity: 98.651
XX
XX alignment_block:
XX US-09-762-491-6 x AAA47701 ..
XX
XX Align seg 1/1 to: AAA47701 from: 1 to: 1873
XX
XX 1 MetSerCysValLysLeuTrpProSerGlyAlaProAlaProLeuValSer 17
XX 165 ATGTCGTGCGTCAAGTTATGAGCCCAAGCGTGCCTCCCTCGTGGTGTCT 214
XX 17 TlleglGluGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 34
XX 215 CATTGAGCAACTGAGACACAGAGCTCTGCTGCCAAAGCGCGGTTCGCA 264
XX 34 hValPheArgAlaGlnHisArgGlyTrpGlyTrpAspValAlaValLys 50
XX 265 CAGTGTTCGGGCGCAACATAGGAAGTGGGCTACGATGGCGGCTCAAG 314
XX 51 lIleValAsnSerLysAlaIleSerArgGluValLysAlaMetAlaSer 67
XX 315 ATCGTAAATCTGAAGCGGATATCCAGAGAGCTCAAGCGCATGCGAGTCT 364

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67 uAspAsnGluPheValLeuAhrGLeuGluGlyValIleGluLysValAsn 84
68 GATTAACGAAATTCGTGCTGCCTAGAGAGGGTTATCGAAGAGGTCGGCG 414
84 rp... AspGlnAspProLysProAlaLeuValThrLysPheMetGluAsn 99
415 GCTGAGGCAAGATCCCAAGCCGGCTCTGCTGATCTAAATTCATGAGAAC 464
100 GlysLeuSerGlyLeuLeuGlnSerGlnCysProArgProTyrProLe 116
465 GGCCTCTGTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
116 uLeuGlyLeuLeuLysGlyValValLeuGlyLysPheTyrLeuHis 133
515 CTTTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
133 spGlnAsnProValLeuLeuHisArgAspLeuLysProSerAsnValLeu 149
565 ACCGAAACCCGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
150 ProAspProGluLeuHisValLysLeuAlaAspPheGlyLeuSerThr 166
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166 eGlnGlyGlySerGlnSerGlyThrGlySerGlyGluProGlyGlyThr 183
665 TCAGGAGGCTCACAGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 714
183 euGlyTyrLeuAlaProGluLeuPheValAsnValAsnArgLysAlaSer 199
715 TGCGCTACTTGGCCCCAGAACGTGTGTGTTAAGCTAAACCGGAGGCTCC 764
200 ThrAlaSerAspValTyrSerPheGlyIleLeuMetTrpAlaValLeuAl 216
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216 eGlyArgGlyValGluLeuProThrGluProSerLeuValTyrGluAla 233
815 TGGAGAGAACTGAGTTCGACCAACCAACCAACCAACCAACCAACCAAC 864
233 aLysAsnArgGlnAsnArgProSerLeuAlaGluLeuProGlnAlaGly 249
865 TGCTCAGCAGGACAGAACCCCTTCATTTGGCTGACCTGCCCAAGCCGG 914
250 ProGluThrProGlyLeuGluGlyLeuLysGlyLeuMetGlnLeuCysTr 266
915 CCTGAGACTCCCGCTTACAGACACTGAAAGAGCTAAATGCAAGCTCTG 964
266 pSerSerGluProLysPheArgProSerPheGlnGluCysLeuProLysTr 283
965 GAGCAGTGAGCCCAAGAGACAGACCTCTTCCAGGAAAGCTTACCAGAAA 1014
283 hrAspGluValPheGlnMetValGluAsnAsnMetCAsnAlaAlaValSer 299
1015 CTGATGAAGTCTTCAGATGTGCGAACAATATGAAATGCTGCTGCC 1064
300 ThrValLysAspPheLeuSerGlnLeuLysSerSerAsnArgArgPhe 316
1065 ACGGTAAAGATTTCTGCTCAGCTCAGACACAGACCAATAGAGATTTTC 1114
316 rLysProGluSerGlyGlnGlyThrGluMetAspGlyPheArgArgTr 333
1115 TATCCAGACTCAGAGCCCAAGAGAGAGCAAAATGATGAGCTTTAGAGAA 1164
333 hrIleGluAsnGlnHisSerArgAsnAspValMetValSerGluTrpLeu 349
1165 CCATAGAAAACACAGCACTCTGTAATGATGATGATGATGATGATGATG 1214
350 AsnLysLeuAsnLeuGluGluProProSerSerValProLysLysCysPr 366
1215 AACCAACTGAAATCTAGAGAGCTCCAGCTCTGTTCTAAATAATGCCCC 1264

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366 oSerLeuThrLysArgSerArgAlaGlnGlnGluGlnValProGlnAlaTr 383
1265 GAGCCTTACCAAGAGAGAGAGGACACAGAGAGAGAGGTTCCACAAAGCT 1314
383 rPThrAlaGlyThrSerSerAspSerMetAlaGlnProProGlnThrPro 399
1315 GGCACAGAGCAGCATCTTCAGATTCATGATGCCCAACCTGCCAGACTCCA 1364
400 GluThrSerThrPheArgAsnGlnMetProSerProThrSerThrGlyTh 416
1365 GAGACCTCAACTTTCAGAAACAGATGCTCAGGCTTACCTCAACTGGAAC 1414
416 rProSerProGlyProArgGlyAsnGlnGlyAlaGluArgGlnGlyMet 433
1415 ACCAAGCTCTGGACCCGAGGAATTCAGGGGCTGAGAGCAAGGACATGA 1464
433 sntPserCysArgThrProGluProAsnProValThrGlyArgProLeu 449
1465 ACTGTCTCTGAGGAGCCCGAGGACCAAAATCCAGTAAAGGCGACGCTC 1514
450 ValAsnIleTyrAsnCysSerGlyValGlnValGlyAspAsnAsnTyrLe 466
1515 GTTAAATATATCAACTGCTCTGGGGTGCAGGTTGGAGAACAACTACTT 1564
466 uThrMetGlnGlnThrThrAlaLeuProThrTrpGlyLeuAlaProSer 483
1565 GACTATGCAACGACAACTGCTTGGCCACATGGGCTTGGCACCTTGG 1614
483 LysGlyArgGlyLeuGlnHisProProProValGlySerGlnGlnGly 499
1615 GCAGGGAGGGGCTTGCACAGACCCCAACAGTAGGTTCGCAAGAAAGGC 1664
500 ProLysAspProGluAlaLeTTrpSerArgProGlnGlyTyrTrpAsnHis 516
1665 CCTAAAGATCTGAAGCTGTGAGAGAGGCCACAGGGTGTGATATATCAT 1714
516 rGlyLys 518
1715 CGGAGAA 1721

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seq_documentation_block:
ID AAD16312 standard; cDNA; 1873 BP.
XX
AC AAD16312;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human kinase of death (KOD) cDNA.
XX
KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
KW cytosolic; ss.
XX
OS Homo sapiens.
XX
FH Key 155..1724 Location/Qualifiers
FT CDS /tag=8 "Human kinase of death (KOD)"
FT /product= "Human kinase of death (KOD)"
FT /transl_except= (pos:411..422, aa: Asn-Trp-Asp)
XX
PD 31-JUL-2001.
XX
PF 21-MAR-2000; 2000US-0531914.
XX
PR 10-JUN-1999; 99US-0329418.
XX
PA (GENE) ZENCA LTD.
XX
PI Gomes BC, Kasof GM, Prosser JC;

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XX WPI: 2001-535022/59.
DR P-PSDB: AAE09430.

XX New human protein activator protein, useful for treating dysfunctional
PT apoptosis conditions and in screening assays to identify agonists which
PT agonize or mimic biological and/or pharmacological activity -

XX Example 3; Column 29-32; 31pp; English.

XX The invention relates to human protein activator of apoptosis and
CC methods to identify compounds that modulate the biological and/or
CC pharmacological activity of the activator and hence regulate
CC apoptosis. The nucleic acid and amino acid sequences of the kinase
CC of death (KOD) are useful for identifying compounds that modulate
CC the biological and/or pharmacological activity of a native mediator
CC of apoptosis, for treating dysfunctional apoptosis conditions, in
CC screening assays to identify agonists which agonize or mimic
CC biological and/or pharmacological activity, induce production of or
CC prolong the biological half-life of the molecule in vivo or in vitro.
CC The present sequence is a cDNA encoding human KOD protein activator
CC of apoptosis.

XX Sequence 1873 BP; 471 A; 531 C; 518 G; 353 T; 0 other:

alignment_scores:
Quality: 2714.50 Length: 519
Ratio: 5.271 Gaps: 1
Percent Similarity: 99.229 Percent Identity: 98.651

alignment_block:
US-09-762-491-6 x MAD16312 ..

Align seg 1/1 to: MAD16312 from: 1 to: 1873

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17 TLeuGluLeuGluAsnGluGluValGlyAspGlyPheGlyTyr 34
215 CATCGAGCACTCGAGACCAAGAGCTGCTCGCAAGGCGGTTCGCA 264
34 hValAlaPheArgAlaGlnHisArgIysTrpGlyTyrAspValAlaValLys 50
265 CAGTGTTCGGGGCGCACTAGAAAGTGGGCTACGATGTGGCGTCAG 314
51 TLeuValAsnSerIysAlaIleSerArgGluValLysAlaMetAlaSerLe 67
315 ATCGTAACTCGAAGCGCATTCACAGGAGTCGAAGCCATGCGCAAGTCT 364
67 uAspAsnGluPheValLeuArgLeuGluGlyValTLeuLysValAsnT 84
365 GGAATACGAATTCGTCTGCGCTAGAAAGGCTTATCGAAGAGTGGCG 414
84 TP...AspGlnAspProLysProAlaLeuValThrLysPheMetGluAsn 99
415 GCTCGAGCCCAAGATCCAAAGCGGCTGTGCTCAAAATTCATGGAAGAC 464
100 GlySerLeuSerGlyLeuLeuGlnSerGlnCysProArgProTyrProLe 116
465 GGGTCTCTGTGCGGGCTGCTGAGTCCAGTCCCTCGGCCCTGGCGCT 514
116 uLeuCysArgLeuLeuLysGluValValLeuGlyPhePheTyrLeuIle 133
515 CMTTTCGCGCTCTCGAAGAACTGTCTGTGCAATGTTTAACTGCAAG 564
133 spGlnAsnProValLeuLeuHisArgAspLeuLysProSerAsnValLeu 149
565 ACCGAAACCCGGGTCTGTGACCGGAGCTCAAGCCATTCAGAGTCTG 614
150 ProAspProGluLeuHisValLysLeuAlaAspPheGlyLeuSerThrPh 166
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615 CTGGACCCAGAGCTGACGTCAGCTGCGAGATTTGGCTGTCCACATT 664
166 eGlnGlyGlySerGlnSerGlyThrGlySerGlyValProGlyTyrThr 183
665 TCAAGGAGCTCACAGTCAAGGACAGGTCGGGAGCCAGGAGGACCC 714
183 euGlyTyrLeuAlaProGluLeuPheValAsnValAsnArgLysAlaSer 199
715 TGGCTACTTGGCCCCAGAACTGTTGTTAACTGAACCGAAGGCTCC 764
200 ThrAlaSerAspValTyrSerPheGlyIleLeuMetTrpAlaValLeu 216
765 ACAGCACTGACGTCTACACTTCGGGATCTCAATGTGGAGTGGCTTC 814
216 aGlyArgGluValGluLeuProThrGluProSerLeuValTyrGluAla 233
815 TCGAAGAAAGTGAAGTTCGCAACGAACTATCATCTGTGACGAGCAG 864
233 aICysAsnArgGlnAsnArgProSerLeuAlaGluLeuProGlnAlaGly 249
865 TGTCCAAAGCAGCAACCGGCTTCATTGGCTGAGCTGCCCAAGCCGG 914
250 ProGluThrProGlyLeuGluGlyLeuLysGluLeuMetGlnLeuCysTr 266
915 CCTGAGACTCCCGGCTTGAAGAGCTGAAGAGCTAATGACGCTGTG 964
266 PserSerGluProLysAspArgProSerPheGlnGluCysLeuProLys 283
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1215 AACCAACTGATCTAGAGAGCGCTCCAGCTCTGCTCTAAAAAAATGCC 1264
366 oSerLeuThrLysArgSerArgAlaGlnGluGluGlnValProGlnAla 383
1265 GAGCTTATCCAAAGACGACGAGCCCAAGAGAGCAGCTTCCAAAGCT 1314
383 TrpThrAlaGlyThrSerSerAspSerMetAlaGlnProGlnThrPro 399
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KW Human; protein kinase; cell growth; tumour; cancer; immune;
KW inflammatory; respiratory; haematological; bone disorder; ds.
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PD 04-JAN-2001.
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PR 30-JUN-1999; 99US-0345473.
PR 01-MAY-2000; 2000US-0562480.
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PA (MIL-) MILLENNIUM PHARM INC.
XX
PI Hodge MR, Meyers R, Williamson M.
XX
DR WPI: 2001-061977/07.
XX
PT New protein kinase polypeptides, nucleic acids and anti-kinase
PT antibodies, useful for diagnosing and treating e.g. cancer,
PT inflammatory, immune, cardiovascular and bone disorders -
XX
PS C1alm 1; F1g 10; 93PP; English.
XX
CC The present invention relates to human protein kinase. The proteins
CC are from human genes termed h12832, h14138, h14813, h15990,
CC h15993, h16341 and h2252. The proteins may be used to identify
CC modulators of their activity. The proteins may also be used to derive
CC products for the treatment of cellular growth related disorders,
CC malignancies, cancers, immune, inflammatory, respiratory,
CC haematological and bone-related disorders.
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alignment_block:
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XX Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX PT useful for preventing, diagnosing and/or treating cancers and
XX PT metastasis -
XX

PS Disclosure: SEQ ID NO 25225; 3071pp + Sequence Listing; English.
XX
XX AAK64951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK67694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
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seq_documentation_block:
ID: NAF30546 standard; cDNA: 1437 BP.
XX
AC: AAF30546;
XX
DE: 28-MAY-2001 (first entry)
XX
Rat RIP-3-like death-associated kinase (R3DAK) cDNA.
DE
RIP-3-like death-associated kinase; R3DAK; rat; antibacterial;
viral;
virucide; protosacide; cardiac; antiinflammatory; vasotropic;
antidiabetic; antitumor; analgesic; immunosuppressive;
antituberc; anticancer; nephrotropic; cyostatic; nootropic;
anticonvulsant; hepatotropic; antiallergic; antigenic;
dermatological; osteopathic; antiallergic; uropathic;
ophthalmological; antiparkinsonian; antispasmodic; neuroprotective;
pulmonary; hormonal; apoptosis; gene therapy; vaccine; ss.
XX
Rattus sp.
XX
MO200119990-AL.
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PD 22-MAR-2001.
XX
PF 15-SEP-2000; 2000MO-0525201.
XX
PR 17-SEP-1999; 99US-0154422.
XX
PA (IMMUNEX CORP.
XX
PI VANCE GD, BIRD TA;
XX
DR WPI: 2001-244803/25.
XX
P-PSDB; AAB20345.
XX
DR
XX
The present sequence is that of the coding region of cDNA encoding
rat RIP-3-like-death-associated kinase (R3DAK, see AAB20345), a
member of the RIP3 family, which is known to be involved in
apoptosis. The cDNA was obtained from a rat dermal papilla cell
library. The invention provides R3DAK polypeptides and
polynucleotides, expression vectors, recombinant host cells, and
methods of producing a recombinant R3DAK polypeptide, as well as
antibodies, a method of designing an R3DAK inhibitor on the basis
of the 3-dimentional structure of a R3DAK polypeptide, a method of
identifying compounds that alter R3DAK kinase activity, and for
using such compounds. R3DAK, its fragments, variants, antagonists,
agonists, antibodies and binding partners are useful for treating:
bacterial, viral or protozoal infections; cardiovascular disorders
such

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as myocardial infection, heart failure, or vacuulitis; solid tumours;
 chronic pains; endocrine system disorders such as diabetes;
 hypothyroidism and thyroiditis, including Hashimoto's thyroiditis;
 gastrointestinal diseases such as Crohn's disease and ulcers;
 genitourinary system disorders such as glomerulonephritis; hematologic
 and oncologic disorders such as cancer; lymphoproliferative disorders
 such as Hodgkin's disease; hereditary conditions such as Gaucher's and
 Huntington's disease; liver disorders such as hepatitis; non-arteritic
 medical conditions of the bones and joints; pulmonary disorders such as
 cystic fibrosis; allergies; rheumatic disorders such as systemic lupus
 erythematosus, gout, osteoarthritis, Reiter's disease;
 graft-versus-host disease; female reproductive system disorders; and
 diseases such as multiple sclerosis, Parkinson's disease, Sjogren's
 disease. R3DK is useful for effecting bodily characteristics,
 diorchyisms or cardiac cycles or rhythms; effecting the fertility of
 male or female subjects; effecting the metabolism, catabolism,
 anabolism, processing, utilization, storage or elimination of dietary
 fat, lipid, polypeptide, carbohydrates, vitamins, minerals, cofactors
 or other nutritional factors or component(s); effecting behavioural
 characteristics; providing analgesic effects or other pain reducing
 effects; promoting differentiation and growth of embryonic stem cells
 in lineages other than haematopoietic lineages; hormonal or endocrine
 activity; treatment of hyperproliferative disorders;
 immunoglobulin-like activity; and the ability to act as an antigen in a
 vaccine composition. Nucleic acids encoding R3DK are useful for
 diagnostic purposes, for expressing recombinant polypeptide for
 analysis, characterisation or therapeutic use, as markers for tissues
 in which the corresponding polypeptide is preferentially expressed,
 to compare with endogenous DNA sequences in patients to identify
 potential genetic disorders; as an antigen to raise anti-DNA
 antibodies or elicit another immune response; and for gene therapy.

Sequence 1437 BP: 368 A: 359 C: 399 G: 311 T: 0 other:

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Align beg 1/1 to: MAF30546 from: 1 to: 1437

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33 LyrThrValPheArgAlaGlnHisArgLysTrpGlyTyrAspValAlaVal 49
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50 LysIleValAsnSerLysAlaIleSerArgLysValLysAlaMetAla 66
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83 SerThrAspGlnAspProLysProAlaLeuValThrLysPheMetGluAsn 99
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ID AAK57466 standard; cDNA; 939 bp.
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AC
XX 06-NOV-2001 (first entry)
DE Human Immune/hematopoietic antigen encoding cDNA SEQ ID NO:2526.
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XX Human; Immune; haematopoietic; Immune/hematopoietic antigen; cancer;
XX cytosolic; gene therapy; vaccine; metastasis; ss.
XX Homo sapiens.
XX
XX MO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
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XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
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XX 02-MAR-2000; 2000US-0186350.
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PR 17-NOV-2000; 2000US-0249217.
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 PR 08-DEC-2000; 2000US-0251989.
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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

XX (HOMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Barash SC, Ruben SM;

XX DR MPI; 2001-465460/50.

XX P-PSDB; AAU17293.

PT Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders

XX Claim 1: SEQ ID NO 245; 880bp; English.

XX The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, hemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC abnormalities (Down syndrome), ischemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). AA526576-AA527850 represent novel signal transduction
 CC pathway protein coding sequences and PCR primers of the invention.

XX alignment_scores:

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 Ratio: 4.428 Gaps: 3
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XX AAK92320;

XX 06-NOV-2001 (first entry)

XX Human cDNA 5'-end sequence, SEQ ID NO: 780.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.
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XX EP130094-A2.
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XX 05-SEP-2001.
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XX 07-JUL-2000; 2000EP-0114089.
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XX 08-JUL-1999; 99JP-0194486.
XX 11-JAN-2000; 2000JP-0118774.
XX 02-MAY-2000; 2000JP-0183765.
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XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2001-524255/58.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
XX Claim 2: SEQ ID NO 780; 1380bp + sequence listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
XX molecules have been determined. Primers for synthesizing the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesized by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence is the nucleotide
XX sequence of the 5'-end of a cDNA provided in the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.
XX
XX Sequence 665 BP; 147 A; 194 C; 190 G; 130 T; 4 other;

Alignment scores:
Quality: 775.50 Length: 169
Ratio: 4.847 Gaps: 2
Percent Similarity: 94.675 Percent Identity: 93.491

Alignment block:
US-09-762-491-6 x AAK932320 ..

Align seg 1/1 to: AAK932320 from: 1 to: 665

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17 TTGGTGTGLeuGluAsnGlnGluLeuValGlyAspGlyPheLeuTyr 34
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215 CATGAGAAAGTGGAGAACCGAGAGCTGCTGCGCAACAGCGCTGCGCA 264
34 hValPheAtGAlaGlnHisArgGlyTyrPheValAlaValAlaVal 50
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265 CAGGTTCGCGCGCAACATAGCAAGTGGCGCTAGAGTGCCTGCTAG 314
51 TLeuValSerLysAlaIleSerArgGluValLysAlaMetAlaSerLe 67
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315 ATCTTAATCTGAAAGCGATATCCAGGAGGTCAAGCGCATGGCAACT 364
67 uAspAsnGluPheValLeuArgLeuGlnGlyValIleGluLysValAsn 84
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365 GGAATAGGAATTCGTCTGCTGCTAGAGGGTTTCAGAAAGGTGAAC 414
84 tPAspGlnAspProLysProAlaLeuValTyrLysPheMetGlnAsnGly 100
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415 GGGACCAAGATCCCAAGCCGCTCTGTGACTAAATTCTCATGAGAACGCC 464
101 SerLeuSerGlyLeuLeuGlnSerGlnCysProArgProTrpProLeuLe 117
|||||
465 TCCCTGTGCGCGCTGCTGAGTCCAGTCCCTCGCGCCGCGGNTCT 514
117 uCyArgLeuLeuLysGluValValLeuGlnMetPheTyrLeuHisAsp 134
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515 TTGCGCGCTGCTGAAAGAAAGTGGTGTGGATGTTTACCTGCGACGACC 563
134 hAsnProValLeuLeuHisArgAspLeuLysProSerAsnValLeuPro 150
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564 AGAACCCGCTGCTCTGACCGGAGCTTAAGCATACAGTCTCTGCTG 613
151 AspProGluLeuHisValLysLeuAlaAsp.PheGlyLeuSerThrPheG 167
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613 GACCCAGAGCTTGAAGTCAAGCTG...CAGATTTGGCGTGCACATTTTC 660
167 lngly 168
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661 ANGGA 665

seq_name: /SIDSI/gcgdata/hold-geneseq/geneeqn-emb1/NA2001A.DAT:AAK93863
seq_documentation_block:
ID AAK93863 standard; cDNA; 665 BP.
XX
XX AAK93863;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human cDNA clone representative sequence, SEQ ID NO: 2323.
XX
XX Human: full length cDNA; cDNA synthesis: oligo-capping; ss.
XX
XX Homo sapiens.
XX
XX EP130094-A2.
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-0114089.
XX
XX 08-JUL-1999; 99JP-0194486.
XX 11-JAN-2000; 2000JP-0118774.
XX 02-MAY-2000; 2000JP-0183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2001-524255/58.

830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
XX Example 11: SEQ ID NO 2323; 1380bp + sequence listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
XX molecules have been determined. Primers for synthesizing the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesized by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence was used as the
XX representative sequence from a human clone which was used in
XX homology searches to identify the clone.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.
XX

Sequence 665 BP; 147 A; 194 C; 190 G; 130 T; 4 other:

alignment_scores:
Quality: 775.50 Length: 169
Ratio: 4.847 Gaps: 2
Percent Similarity: 94.675 Percent Identity: 93.491

alignment_block:

US-09-762-491-6 x AAF44704

Align seg 1/1 to: AAF44704 from: 1 to: 665

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215 CATGAGAGAACTGGAGACAGAGAGCTGCTGGCAAGCGGGTTGGCA 264
34 hrValPheArGAlaGlnHlaArgLysTrpGlyTyrAspValAlaValLys 50
265 CAGGCTTCCCGCGCAACATAGCAAGTGGGCTACGATGCGCGTCAAG 314
51 IleValAsnSerLysAlaIleSerArgGluValLysAlaMetAlaSerLe 67
315 ATGTAATCACTCAAGCGCATTCACAGGGAGGTCAGAGCCATGCAAGCT 364
67 uAspAsnGluPheValLeuArgLeuGluGlyValIleGluLysValAsn 84
365 GAAATACGAATTCCTGCTCCCTCAAGCGCTTATCCAGAAAGTCAACT 414
84 rPheAspGlnAspProLysProAlaLeuValThrLysPheMetGluAsnGly 100
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101 SerLeuSerGlyLeuLeuGlnSerGlnCysProArgProTyrProLeuLa 117
465 TCTCTGGCGGGCTGCTGCAATCCAGTCCCTCGCGCTGCGGNNCT 514
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564 AGAACCCGGGTCTCTGCACCGGACCTTAAACCATTCACAGCTCTCTG 613
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661 ANSQA 665

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seq_name: /SID1/gcdata/hold-geneseq/geneseqn-cmb1/NA2001A.DAT:AAF44704

seq_documentation_block:

ID AAF44704 standard: cDNA; 1073 BP.

AC AAF44704:

XX 27-MAR-2001 (first entry)

DE Novel protein kinase cDNA, SEQ ID NO: 85.

XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;

KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;

KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;

KW immune disorder; cardiovascular disease; neurodegenerative disease;

KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;

KW Inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

XX Mus musculus.

OS WO200073469-A2.

XX 07-DEC-2000.

XX 26-MAR-2000; 2000MO-US14842.

XX 28-MAR-1999; 99US-0136503.

XX (SUGEN-) SUGEN INC.

XX Plozman GD, Martines R, Whyte D, Sudersanam S;

XX MPI; 2001-03261/04.

XX P-PSDB; AAB65676.

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers -

XX Disclosure: Fig 2; 310pp; English.

XX The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression, such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in diagnostic assays. The kinase polypeptides may also be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, CC immune disorders, cardiomyopathies, strokes, renal failure, CC oxidative-stress related disorders, chronic inflammatory bowel disease, CC chronic inflammatory pelvic disease, multiple sclerosis, asthma, CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and CC reproductive disorders.

Sequence 1073 BP; 296 A; 289 C; 265 G; 223 T; 0 other:

alignment_scores:

Quality: 703.50 Length: 322
Ratio: 3.099 Gaps: 8
Percent Similarity: 70.497 Percent Identity: 50.311

alignment_block:

US-09-762-491-6 x AAF44704

Align seg 1/1 to: AAF44704 from: 1 to: 1073

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209 eleuMetPheAlaValLeuAlaGlyArgGluValGluLeuProThrGluP 226
53 CCTGCTGGGCGAGTCTGCTGCGCAAGAGCTGAGTTGGTACAAACA 102
226 roSerLeuValTyrGluAlaValCysAsnArgGlnAsnArgProSerLeu 242
103 CTTCATATTCGCGGAACAGGTGTGACAGGACGAGCTCTCCACATG 152
243 AlaGluLeuProGlnAlaGlyProGluThrProGlyLeuGluLysLeuTyr 259
153 ACAAGCTGCTCCAGTAGCCCTGAGACTCCCGCTTGAAAACTGAA 202
259 gGluLeuMetGlnLeuCysTrpSerSerGluProLysAspArgProSerP 276

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353 AACCAAGCGCAGAAACTGTCTGCCAGAGCCAGCCAGCAAGAGCAGAC 402
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403 AATGTGATGCCGAGGAAACC..... 425
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473 ACCAGTTCCTGAAATGTCT.....GAGAGCAGACACAG 510
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511 ACACATAGTGGGCTGCGCACACAGCAGAGACATCTGTGACCCCGTG 560
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 seq_name: qb_pat:AR105328
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 LOCUS AR105328
 DEFINITION Sequence 2 from patent US 6096539.
 ACCESSION AR105328
 VERSION AR105328.1 GI:12818925
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1557)
 AUTHORS Gomes,B.Charles., Kasof,G.M. and Prosser,J.Caroline.
 TITLE Protein activator of apoptosis
 JOURNAL Patent: US 6096539-A 2 01-AUG-2000;
 FEATURES
 source 1..1557
 BASE COUNT 395 a 422 c 448 g 291 t 1 others
 ORIGIN
 Alignment_scores:
 Quality: 2744.00 Length: 518

Ratio: 5.328 Gaps: 0
Percent Similarity: 99.421 Percent Identity: 99.228

Alignment block:
US-09-762-491-6 x AR105328

Align seg 1/7 to: AR105328 from: 1 to: 1557

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484 yAGlYArgGlyLeuGlnHlaProProProValGlySerGlnGluPro 500
1451 AGGGAGGGGCTTGACAGACCCCCACAGTATGTTGCGAAGAGGCCCT 1500
501 LysAspProGluAlaTPrSerArgProGlnGlyTPrTyrAsnHlaSerG 517
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1551 GAAA 1554.
seq_name: gb.pat:AX067677
seq_documentation_block:
locus: AX067677 1557 bp DNA linear PAT 19-JAN-2001
DEFINITION Sequence 2 from Patent W00077200.
ACCESSION AX067677
VERSION AX067677.1 GI:12329571
KEYWORDS
SOURCE human.
ORIGIN Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1557)
AUTHORS Gomez,B.C., Kasof,G.M. and Prosser,J.C.
TITLE Receptor interacting protein rip3
JOURNAL Patent: WO 0077200-A 2 21-DEC-2000;
Astrazeneca AB (SE)

FEATURES
source Location/Qualifiers
1..1557

BASE COUNT 395 a 422 c 448 g 291 t 1 others
ORIGIN

alignment_scores: Quality: 2744.00 Length: 518
Ratio: 5.328 Gaps: 0
Percent Similarity: 99.421 Percent Identity: 99.228

alignment_block:
us-09-762-491-6 x AX067677 ..

Align beg 1/1 to: AX067677 from: 1 to: 1557

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ACCESSION AR105327
VERSION AR105327.1 GI:12818924
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1873)
AUTHORS Gomes,B,Charles., Kasof,G.M. and Prosser,J.Caroline.
TITLE Protein activator of apoptosis
JOURNAL Patent: US 6096539-A 1 01-AUG-2000;
FEATURES
source 1..1873
location/Qualifiers
BASE COUNT 471 a 531 c 518 g 353 t
ORIGIN

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DEFINITION Sequence 1 from Percent W00077200.
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VERSION AX067676.1 GI:12329570
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Gomes B.C., Kasof G.M. and Prosser J.C.
TITLE Receptor interacting protein rlp3
JOURNAL Percent: W0077200-A 1 21-DEC-2000;
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Location/Qualifiers
BASE COUNT 471 a 531 c 518 g 353 t
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seq_documentation_block: 1437 bp DNA linear PAT 02-APR-2001

LOCUS AX100029

DEFINITION Sequence 1 from Patent WO0119990.

ACCESSION AX100029

VERSION AX100029.1 GI:13539035

KEYWORDS

SOURCE

ORGANISM

Rattus sp.

Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 1437)
 AUTHORS Virca, C.D. and Bird, T.A.
 TITLE RLP-3-like death-associated kinase
 JOURNAL Patent: WO 011990-A 1 22-MAR-2001;
 IMMUNEX CORPORATION (US)
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 location/Qualifiers
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Consensus quality: 239918 bases at least Q30
Consensus quality: 240258 bases at least Q20
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Insert size: 244684; sum-of-contigs
Quality coverage: 7.64 in Q20 bases; agarose-fp
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* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record
* arbitrary. Gaps between the contigs are represented
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
* as soon as it is available and the accession number
* be preserved.
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ACCESSION AX056439
VERSION AX056439.1 GI:12229146
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE
1 (bases 1 to 1073)
AUTHORS PLOWMAN,G.D., MARTINEZ,R., WHYTE,D. and SUDERSANAM,S.
TITLES Protein kinases
JOURNAL Patent: WO 0073469-A 83 07-DEC-2000;
Sugen, Inc. (US)
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DEFINITION Mus musculus cell death protein (RIP) mRNA, complete cds.
ACCESSION U75995
VERSION U75995.1 GI:829618
KEYWORDS Fas; TNF receptor.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (Phases 1 to 2368)
TITLE Stanger, B.Z., Leder, P., Lee, T.H., Kim, E. and Seed, B.
RIP: a novel protein containing a death domain that interacts with
Fas/p50-1 (CD95) in yeast and causes cell death
JOURNAL Cell 81 (4), 513-523 (1995)

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MEDLINE      95277838
REFERENCE    2 (bases 1 to 2268)
AUTHORS      Stanger,B.2.
TITLE        Direct Submission
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              School, 200 Longwood Avenue, Boston, MA 02115, USA
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232 TTGGAAAGAGGGAGATGATACACAGACAGACACATCGACGTGGTGA 281

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TITLE Protein kinase C-associated kinase (PKC), a novel
membrane associated, ankyrin repeat-containing protein kinase
JOURNAL J. Biol. Chem. 276 (24), 21737-21744 (2001)
MEDLINE 21293027
PUBMED 11278382

REFERENCE
AUTHORS 2 (bases 1 to 3559)
TITLE Chen, L., Halder, K., Carlappa, A. and Pillai, S.
JOURNAL Direct Submission
SUBMITTED (01-SEP-2000) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
3 (bases 1 to 3559)
AUTHORS Chen, L., Halder, K., Carlappa, A. and Pillai, S.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
REMARK
AUTHORS Sequence update by Submitter
TITLE 4 (bases 1 to 3559)
AUTHORS Chen, L., Halder, K., Carlappa, A. and Pillai, S.
JOURNAL Direct Submission
SUBMITTED (08-JAN-2002) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
REMARK
COMMENT Nucleotide sequence update by submitter
REMARKS On Jan 8, 2002 this sequence version replaced g1:18086161.
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BASE COUNT 826 a 900 c 1000 g 833 t
ORIGIN

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1776 TGCACATGCTGCTGCTGCGAGGCCAC 1801

seq_name: gb_pat:ARI45196
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LOCUS ARI45196 2016 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6211337.
ACCESSION ARI45196
VERSION ARI45196.1 GI:15107063
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2016)
AUTHORS Batchval,V.R., Huang,J., Hsu,H. and Goeddel,D.V.

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TITLE RIP: novel human protein involved in tumor necrosis factor signal
JOURNAL transduction
Patent: US 6211337-A 1 03-APR-2001;
FEATURES Location/Qualifiers
source 1..2016
BASE COUNT 629 a 446 c 514 g 427 t
ORIGIN

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REFERENCE 1 (bases 1 to 1026)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
 DNA Sequencing by: Incyte Genomics, Inc.
 clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at:
<http://image.llnl.gov>
 Plate: LML1159 row: k column: 19
 High quality sequence stop: 860.
 Location/Qualifiers

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 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector: pCRV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed and Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library"

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 US-09-762-491-6 x B1819557 ..

Align seg 1/1 to: B1819557 from: 1 to: 1026

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VERSION B1838468.1 GI:15950018
KEYWORDS EST.
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 897)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at:
http://image.llnl.gov
Plate: LML1159 row: b column: 13
High quality sequence stop: 888.

```

FEATURES

Location/Qualifiers

1..897
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:522316"
 /clone_lib="NIH_MGC_120"
 /lab_host="DH10B"
 /note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC library."

BASE COUNT 193 a 263 c 266 g 175 t
 ORIGIN

alignment_scores:
 Quality: 1159.00 Length: 250
 Ratio: 4.770 Gaps: 1
 Percent Similarity: 97.200 Percent Identity: 96.400

alignment_block:
 US-09-762-491-6 x B1839468 ..

Align beg 1/1 to: B1838468 from: 1 to: 897

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1 MetSerGyVallyLeuTProSerGlyAlaProAlaProLeuValSe 17
143 ATGTCGTCGCTCAAGTATGCGCCAGCGGTGCCCCCTGGTGGTGC 192
17 TTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 34
193 CATCGAGAACTGGAACAGAGAGCTGCTGGCAAGAGCGGTGGCA 242
34 hTVALPHEATGALAGLHLAGATGATGATGATGATGATGATGATG 50
243 CAGTGTTCGGGGCCAGCATGAGAGAGAGAGAGAGAGAGAGAGAG 252
51 TLEVALNSERLYSALALIESATGCTGATGATGATGATGATGATG 67
293 ATCTTAATCTGAAAGCGATATCTCAGGAGCTCAAGCGCATGCT 342
67 uAPASNGIuPhValLeuArgLeuGluGlyValTLeGluuValAsn 84
343 GGAATACGAATTCGTGCTGCGCTAGAGGGCTTATCGAAGAGTGA 392
84 rPAAGGInaAPProLySPROAlaLeuValTThrLYSPHemETGUA 100
393 GGGACCAAGATCCCAAGCCGCTGCTGATCAATTAATGAGAACGG 442
101 SerLeuSerGlyLeuLeuGlnSorGlnCysProATGProTProLe 117
443 TCTTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
117 uCYAArgLeuLeuLYsGluValValLeuGluWhePheTyrLeuL 134
493 TTGGCGGCTGCTGAAAGAGTGTGTTGATGTTTAACTGTCACAC 542
134 InaAPProValLeuLeuHsArgAPLeuLYSPROSerAsnValLe 150
543 AGAACCCGGTCTGCTGACCGGAGCTCAACCCATCCAACTCTCT 592
151 ASPProGluLeuHsValLYsLeuAlaAPPhEGlyLeuSerThrPh 167
593 GACCCAGAGCTGACGTCAGCTGCGCATTTTGGCTGCTCAATTT 642
167 nGLYGLYSerGlnSerGlyThrGlySerGlyValProGlyVal 183
643 GGGAGGCTCAACAGTCAGAGGAGAGGCTCGGGAGACCAAGGG 652

```

```

184 GtYrTLeuAlaProGluLeuPheValaLeuValaLeuArgLYsAla 200
693 GGCTACTGGCCCGAAGCTGTTGTTAAAGTAAACCGAAGGCTCCAC 742
200 rALSerAPValTyrSerPheGlyTLeuMetTrrPALaValLeuAla 217
743 AGC.AGTACGCTACAGCTTCGGATCCTAATGTGGCAGTCTGCTG 791
217 LYAGGluValGluLeuProThrGluProSerLeuValTyrGluAla 233
792 GAAGGAAAGTTGAGTTCACAC.GAACCATCATCGGTGCGAAGCAG 840
234 CysAnArgGlnaAnArgProSerLeuAlaGluLeuProGlnAlaG 249
841 TCCACACAGCAGAACCGGCT.TCCTTGGCTGAGCTGCCAAGCCGG 887

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seq_name: gb_cst2:B1823411

seq_documentation_block:
 LOCUS B1823411 922 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603041149F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5181972 5',
 mRNA sequence.
 ACCESSION B1823411
 VERSION B1823411.1 GI:15934961
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 922)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgrahbs-remail.nih.gov
 Tissue procurement: life technologies, inc.
 CDNA library preparation: life technologies, inc.
 CDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL1454 row: a column: 13
 High quality sequence start: 2
 High quality sequence stop: 785.

FEATURES

Location/Qualifiers

1..922

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5181972"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC library."

BASE COUNT 206 a 269 c 270 g 177 t
 ORIGIN

alignment_scores:
 Quality: 1099.50 Length: 252
 Ratio: 4.659 Gaps: 8
 Percent Similarity: 93.651 Percent Identity: 92.063

alignment_block:

US-09-762-491-6 x B1823411

Align seg 1/1 to: B1823411 from: 1 to: 922

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1 MetSerCysValIysLeuTrpProSerGlyAlaProLeuValSe 17
|||||
173 ATCTCTGGGTCAAGTTATGCGCCGCGGTGCCCCCGCTGGGTGTC 222
17 rTlglugluLeuGluAsnGlnGluValGlyIysAspGlyPheGly 34
|||||
223 CATCGAGGAAGTGGAGAACCAAGACCTGTCGCGAAAGCCGGTCCGCA 272
34 hValAlaPheArgAlaGlnHisArgGlyTrpGlyTyrPheValAlaValIys 50
|||||
273 CAGTCTCCGGCGGCACATGACGAGTGGCTGATGATGCGGTCAAG 322
51 lIeValAsnSerLysAlaIleSerArgIuValIysAlaMetAlaSerLe 67
|||||
323 ATCGTAACTCGAAGCGGATATCCAGCGAGGTCAAGGCCATGCCACTCT 372
67 uAspArgGluPheValIleuArgLeuGluGlyValIleGluIysValAsn 84
|||||
373 GGTATACGAATTCGTGCTGCGCTGAGAGGGTTATCCAGAGGTGACT 422
84 rPheArgIleAspProIysProAlaLeuValIThrLysPheMetGluAsnGly 100
|||||
423 GGCACCAAGATCCAGACCGCCTGTGCTGACTAATCATGAGAACGGCC 472
101 SerLeuSerGlyLeuLeuGlnSerGlnCysProArgProTrpProLeuLe 117
|||||
473 TCCTGTGCGGGGTGCTGCTGAGTCCAGTGGCCTGGCGCTGCGCTCC 522
117 uCysArgLeuLeuIysGluValIleValLeuGlyMetPheLysLeuHisArg 134
|||||
523 TTGCGCGCTGCTGAAAGAGTGTGCTGGGATGTTTACCTGACAGACC 572
134 lAsnArgValIleuLeuHisArgAspLeuLysProSerAsnValIleuPro 150
|||||
573 AGAACCCGCTGCTCCGTCACCGGACCTCAAGCCATCCAAAGTCCGTC 622
151 AspProGluLeuHisValIysLeuAlaAspPheGlyLeuSerThrPheGly 167
|||||
623 GACCCGACCTGACACTCAAGCTGSCAATTTTGCTGCTCCACATTTCA 672
167 nGlyGlySerGlnSerGlyThrGlySerGlyGluProGlyGlyThrLeu 183
|||||
673 GGGAGGCTCACAGTCAGGAGACGGGTCCGGGAGCCAGGGGCGACCTG 722
184 GlyTyrLeuAlaProGlyIuLeuPheValAlaValAsnArgLysAlaSer 199
|||||
723 GCGTACTGTGCCCAAGACTGCTGTAAAGTAAACGGAAAGGCTCC 772
200 ThrAlaSerAspValTyrSerPheGlyIleLeuMetTrpAlaValIle 215
|||||
773 ACAGCCAGTACGATCTACAGTCTCCGGATCTTAATGTTGGCAAGTCT 822
215 uAlaGlyArgGluValIleGluLeuProThrGluProSerLeuValTyrG 231
|||||
823 TCTGGAAAGAAAGAACGTTGAGTGGCAACCGAAGCATCTGCTGTAAG 872
231 lValIleValCysAsnArgGlnAsnArgProSerLeuValGly 244
|||||
873 AACCCATGTCACAGGGAACCGGGCTTCAATGGCTGA 914

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seg_name: gb_est1:AW959157

seg_documentation_block:

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LOCUS      AW959157                630 bp      mRNA      linear      EST 01-JUN-2000
DEFINITION EST371227 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW959157
VERSION    AW959157.1 GI:8148841
KEYWORDS   EST.
SOURCE     human.

```

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 630)
Hedge, P., Qi, R., Abernathy, R., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J., and Quackenbush, J.

TITLE

Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

JOURNAL

Unpublished (2000)

COMMENT

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 130

FEATURES

Seq primer: Reverse.
Location/Qualifiers

SOURCE

1..630

BASE COUNT

180 a 170 c 164 g 116 t

ORIGIN

1..630

ALIGNMENT_SCORES:

Quality: 1070.00
Ratio: 5.169
Percent Similarity: 98.571
Percent Identity: 96.667

ALIGNMENT_BLOCK:

US-09-762-491-6 x AW959157

Align seg 1/1 to: AW959157 from: 1 to: 630

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284 AspIuValPheGlnMetValGluAsnAsnMetAlaAlaValSerTh 300
2 GATGATGCTTCCAGATGCTGAGAGACATATGATGATGCTGCTCCAC 51
300 rValIysAspPheLeuSerGlnLeuLysSerSerAsnArgAlaGlyPheSer 317
|||||
52 GGTAAAGATTTCTCTCTCAGCTCAGAGAGCAATGAGATGTTTCTA 101
317 lLeProGluSerGlyGlnGlyThrGluMetAspGlyPheArgArgThr 333
|||||
102 TCCAGAGTCAGGCCCAAGAGGAGCAGACAAATGATGATGCTTACAGAAC 151
334 lIleGluAsnGlnHisSerArgAsnAspValIleValSerGluThrLeuAs 350
|||||
152 ATAGAAAACCGACACTCTGCTGTAATGATGCTGATGCTTCTAGAGTAA 201
350 nLysLeuAsnLeuGluGluProProSerSerValProLysLysCysProS 367
|||||
202 CAACCTAATCTAGACAGACCCCTCCAGCTCTGTTCCCTAAATAATCCCG 251
367 eLysuThrLysArgSerArgAlaGlnGluGluGluValProGlnAlaTrp 383
|||||
252 GCGTTACCAAGAGAGACAGCGACAAAGAGAGAGAGTCCACAAAGCTCG 301
384 ThrAlaGlyThrSerSerAspSerMetAlaGlnProProGlnThrProG 400
|||||
302 ACAGCAGGACATCTTCAGATTCATGATGCGCCCAAGCTCCACAGACTCA 351
400 uThrSerThrPheArgAsnGlnMetProSerProThrSerThrGlyThrP 417
|||||
352 GACCTCACTTTCAGAAACAGATGCGACCGCTACCTCACTCACTGGAAC 401
417 rAspArgProGlyProArgGlyAsnGlnGlyValArgGlyGlnGlyMetAs 433
|||||
402 CAATCTCTGAGCCCGAGGAGATCAAGGGGCTGACAGACACAGCATGAA 451

```

434 TtpSerCysArgThrProGluProAnProValThrGlyArgProLeuVa 450
 432 TGGTCCTGACAGAGACCGGAGCCAAATCCAGTACAGGAGCGCTCGT 501
 450 TAsnIleGlyTrpAsnCysSerGlyValAlaValAspAsnAntytleut 467
 502 TAACTATATACAACTGCTGTGGGTGCMAATGTGAGACAACTACTGA 551
 467 hTMeGlnGlnThrThrAlaLeuProThrTrpGlyLeuAlaPro.SerGI 483
 532 CTATCAACACAGACACTGCTGTGGCCAAAGGCGTTCGACCTTTCGGG 601
 483 yLyseGlyArgGlyLeuGlnHisProPro 492
 602 CCAAGGAGAGGGGTTCGCAACCCCGCC 639

seq_name: gb_estc2:BF001916

seq_documentation_block:

LOCUS BF001916 643 bp mRNA linear EST 06-OCT-2000
 DEFINITION 795c10.x1 NCI-CGAP-Co16 Homo sapiens CDNA clone IMAGE:3314226 3'

ACCESSION BF001916 similar to TR:Q9Y572 Q9Y572 RIP-LIKE KINASE.; mRNA sequence.

VERSION BF001916.1 GI:10702191

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 643)
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL Tumor Gene Index
 Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgep@bcrfemail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
 Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNT, send email to:

info@image.llnl.gov

Seq primer: -40bp from G1bco

High quality sequence stop: 166.

FEATURES

source

Location/Qualifiers

1..843

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3314226"

/clone_11b="NCI-CGAP-Co16"

/tissue_type="colon tumor, RER"

/lab_host="DH10B"

/note="Organ: colon; Vector: pUT3D-Pac (Pharmacia) with a
 modified polylinker; Site: 1: Not 1; Site: 2: Eco RI;
 plasmid DNA from the normalized library NCI-CGAP-Co16 was
 prepared, and 89 clones were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clonoids 1057416-1061255, and 1144584-1145311).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 129 a 166 c 162 g 186 t

ORIGIN

alignment_scores:
 Quality: 927.50 Length: 234
 Ratio: 4.831 Gaps: 2
 Percent Similarity: 82.051 Percent Identity: 76.068

alignment_block:

US-09-762-491-6 x BF001916/rev ..

Align seg 1/1 to reverse of: BF001916 from: 1 to: 643

286 ValPIeGlnMetValGluAsnAsnMetAsnAlaValSerThrVally 302
 643 GTCCTCAAGATGTCGACACTAATATCAATGCTGGGCTTACACGTA 594
 302 sApPheLeuSerGlnLeuLysSerSerAsnArgArgPheSerIleProG 319
 593 GGATTTCTCTGATATCGTTACAGACAGCAATATGAGATGTATATCC 544
 319 JuSerGlyGlnGlyThrGlnMetSerPlyPheArgArgThrIle 335
 543 ACACAGATCTAGAGGACACACATATGATGCTCTAGAGGATATGTT 494
 336 AaGlnHisSerArgAsnAspValMetValSerGluTrpLeuAsnLysLe 352
 493 AACCAAGACTCTCGTAATGATGTCATGTTCTGAGTGTAAACATCTG 444
 352 uAsnLeuGluGluProProSerSerValProLysLysCysProSerLeu 369
 443 ACATGTAGAGGAGCCCTCCAGTTCTGTCTTAATATATGCCGAGCTTA 394
 369 hTrpArgSerArgAlaGlnGluGlnValProGlnAlaTrpThrAla 385
 393 CCAAGAGAGCAGGACACAAAGAGCAGGTTCCACACACCTCGACACCA 344
 386 GlnTrpSerSerAspSerMetAlaGlnProProGlnThrProGlnThrSe 402
 343 GCACATCTTCAGATATGATGCGCCACCACTCCCACTGCA..... 302
 402 rThrPheArgAsnGlnMetProSerProThrSerThrGlyThrProSerP 419
 302 302
 419 rodIyProArgGlyAsnGlnGlyAlaGluArg.GlnGlyMetAsnTrpSe 435
 301GAGCAAGGCACTGAACTGGTC 281
 435 rCysArgThrProGluProAnProValThrGlyArgProLeuValAsnI 452
 280 CTGACAGAGCCCGGAGCCAAATCCAGTAACAGGCGACCGCTGTACCA 231
 452 tETrpAsnCysSerGlyValAlaValGlyAspAsnAsnTytleuthrMet 468
 230 TATACACTGCTCTGGGGTGCATGTTGAGACACACACTTGGCTATG 181
 469 GlnGlnThrThrAlaLeuProThrTrpGlyLeuAlaProSerGlyLysGI 485
 180 CAACAGACAACTGCTGCCCATGCGCTTGCACCTCGCGCAACGCG 131
 485 yArgGlyLeuGlnHisProProProValGlySerGlnGluGlyProLysA 502
 130 GAGGGGCTTCAGACACCCCCACCATAGTTTCGCAAGAAGCCCTAAG 81
 502 sProGlnAlaTrpSerArgProGlnGlyTrpTyAsnHisSerGlyLys 518
 80 ATCTGAAAGCTTGAGAGGACGACAGGTTGATTAATCATATAGCGGAAA 31

seq_name: gb_estc1:AL601137

seq_documentation_block:

LOCUS AL601137 758 bp mRNA linear EST 14-AUG-2001
 DEFINITION DKFZ31300939.r1 313 (aynonym: hlc2) Homo sapiens CDNA clone

ACCESSION AL601137 DKFZ31300939 5', mRNA sequence.

VERSION AL601137.1 GI:15164643

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 758)
 AUTHORS Duesterhoeft, A., Lauber, J., Meves, H.W., Casenhuber, J. and Wiemann, S.
 TITLE EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Duesterhoeft A
 MIRS

Am Klopferstr. 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by Oligen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 3' sequence available.
 This clone (DKFZ31300939) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
 FEATURES
 SOURCE 1..758
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZ31300939"
 /clone_id="313 (synonym: hlcz2)"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pT7Blue2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

BASE COUNT 167 a 231 c 211 g 145 t 4 others
 ORIGIN

alignment_scores:
 Quality: 804.50 Length: 173
 Ratio: 4.905 Gaps: 1
 Percent Similarity: 94.798 Percent Identity: 91.329

alignment_block:
 US-09-762-491-6 x AL601137 ..

Align seg 1/1 to: AL601137 from: 1 to: 758

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1 MetSerCyValLysLeuTrpProSerGlyAlaProAlaProLeuValSe 17
192 ATCTCTGCGCTCAAGTTATGCGCCGCGCCGCGCCCTTCGCTGC 241
17 TTAGGUGUUGUUAAGUGUAGUGUAGUAGUAGUAGUAGUAGUAGUAG 34
242 CATCGAGAACTGCGAACCAAGACGCTGCGCGAAAGCGGTTGCGCA 291
34 hValAlaPheArgAlaGlnHisArgLysTrpGlyTyrAspValAlaValLys 50
292 CAGTGTTCGGGGCGCCACATAGGAAGTGGGCTACGATGCGCGCTCAAG 341
51 lLeValAsnSerLysAlaIleSerArgLysValLysAlaMetAlaSerLe 67
342 ATCGAAACTCGAAGGCGATATCGAGGAGCTCAAGGCCATCGCAAGTCT 391
67 uAspArgLysPheValLeuArgLysGlyValIleGlnLysValAsnT 84
392 GGTAAACGAAATTCGTGCTGCGCTAGAGGGGTTATGGAAGAAGGTGAAC 441
84 tPAspGlnAspProLysProAlaLeuValIleTrpLysPheMetGluAsnGly 100
442 GGGACCAAGATCCCAAGCGCGCTGTGTGACTAAATTCAATGAGAAACCG 491
101 SerLeuSerGlyLeuLeuGlnSerGlnCySerProArgProTrpProLeu 117
492 TCCCTTTCGGGGCTGCGAGTCCAGTCCAGTCCGCGCCCTGCGCGCTCT 541
117 uCyAsnGluLeuLysGluValValLeuGlnMetPheTyrLeuHisAspG 134
542 TTGCGCGCTGCTGAAAGAGTGTGCTGGGATGTTTACCTCGACAGACC 591
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134 lAsnProValLeuHisArgAspLeuLysProSerAsnValLeuPro 150
 592 AACAACCGGCTCTCTGCACCGGAGACCTCAAGCCATCCACAGCTGCGCG 641
 151 AspProGluLeuHisValLysLeuAlaAspPheGlnLysSerThrPheAl 167
 642 GACCCAGAGCTGACGTCAGAGTCACG.....TCGTTCACACCCCT 682
 167 nGlyLysSerGlnSerGly 173
 683 CTCAGCTCAAGCAAGC 701
 seq_name: gb_est2:BI905455

seq_documentation_block:
 LOCUS BI905455 906 bp mRNA linear EST 16-OCT-2001
 DEFINITION 603167947P1 NCI-CGAP_Lu33 Mus musculus cDNA clone IMAGE:5256010 5',
 mRNA sequence.
 ACCESSION BI905455
 VERSION BI905455.1 GI:16167978
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 906)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rtmail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 plates: LMNL1646 row: n column: 11
 High quality sequence start: 28
 High quality sequence stop: 807.
 Location/Qualifiers
 FEATURES
 SOURCE 1..906
 /organism="Mus musculus"
 /strain="C2ECH 11"
 /db_xref="taxon:10090"
 /clone_image="5256010"
 /clone_id="NCI-CGAP_Lu33"
 /tissue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAATGAGAGAGGCGCCCTCTTTTCTTTTCTTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 188 a 245 c 265 g 208 t

alignment_scores:
 Quality: 780.50 Length: 231
 Ratio: 3.771 Gaps: 5
 Percent Similarity: 82.470 Percent Identity: 70.120

alignment_block:
 US-09-762-491-6 x BI905455 ..

|||||
 462 TCCCTGCGGGCTGCTCCAGTCCCTGCGCCCTGCGCTCT 511
 117 UCyAaTgLeuLysGluValLeuGlyMetPheTyrLeuHsAspG 134
 512 TTGGCGCTCTCTGAAGAAGTGGTCTGGATGTTTACCTGCAGCAGC 561
 134 LnaaNPoVallLeuHsAspAspLeuLysProSerAsnValLeuPro 150
 562 AGAACCGGTCCTGCTGCACCGGAGCTCAACCATCCACGCTCTGCTG 611
 151 Asp 151
 612 GAC 614

seq_name: gb-est1:AA227673

seq_documentation_block:

LOCUS AA227673 440 bp mRNA linear EST 06-AUG-1997

DEFINITION z55d09.r1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667313

5' mRNA sequence.

ACCESSION AA227673

VERSION AA227673.1 GI:1849253

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 440)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,

Schellenberg, K., Stepien, M., Tan, F., Thelning, B., White, Y., Wyllie,

T., Watson, R., and Wilson, R.

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LUML; contact the

IMAGE Consortium (info@image.lumc.gov) for further information.

Insert length: 829 Std Error: 0.00

Seq primer: 28m13 rev7 ET from AmerSham.

Location/Qualifiers

1. 440

/organism="Homo sapiens"

/db_xref="GeneID:5561280"

/db_xref="taxon:9606"

/clone="IMAGE:667313"

/clone_11b="Scores_NHMPu_S1"

/library="type="Pooled human melanocyte, fetal heart, and

pregnant uterus"

/lab_host="DH108"

/note="Organ: mixed (see below); Vector: p7730-Pac

(Pharmacia) with a modified polylinker; Site: 1: Not 1;

Site 2: Eco RI; Equal amounts of plasmid DNA from three

normalized libraries (melanocyte 2NDM, pregnant uterus

NBHPU, and fetal heart NBH1W) were mixed, and 88 clones

were made in vitro. Following NBP purification, this DNA

was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from pools of

5,000 clones made from the same 3 libraries. The pools

consisted of 1.M.A.G.E. clones 26032-265223,

340488-345479, and 484488-489479."

BASE COUNT 131 a - 119 c 111 g 79 t

ORIGIN

alignment_scores:

Quality: 760.00

Ratio: 5.278

Length: 145

Gaps: 0

Percent Similarity: 99.310 Percent Identity: 99.310

alignment_block:

US-09-762-491-6 x AA227673 ..

Align seg 1/1 to: AA227673 from: 1 to: 440

315 PhesRtIleProGluSerGlyGlnGlyTyrGluMetAspGlyPheAr 331
 5 TTTTATATCCCAAGTCAAGCCCAAGAGGAGCAAGAAATGATGGCTTAA 54
 331 gArGThrIleGluAngIHisSerArgAsnAspValMetValSerGluT 348
 55 GAGAACATATAGAAACCAAGCAGCTCTGATATGATCTATGTTCTGAGT 104
 348 rPLeuAsnLysLeuAsnLeuGluGluProProSerSerValProLysLys 364
 105 GGCTAAACAAACTGATCTAGAGAGAGCTCCAGCTGTCTCTTAAAAAA 154
 365 cysProSerLeuThrLysArgSerArgAlaGlnGluGlnGluValProG 381
 155 TCCCGAGCCCTTACCAAGAGAGAGAGGA.CAAGAGAGAGAGTTCCACA 203
 381 nAlaTrpThrAlaGlyThrSerSerAspSerMetAlaInProGlnT 398
 204 ACCCTGAGACAGCAGCAGCATCTTCAATTCGATGCGCCCACTCCAGCA 253
 398 hPProGluThrSerThrPheArgAsnGlnMetProSerProThrSerThr 414
 254 CTCACAGACACTCACTTTCAGAAACACATCCAGCCCTCACTCACT 303
 415 GlyThrProSerProGlyProArgGlyAsnGlnGlyAlaGluArgGln 431
 304 GGAACACCAAGTCTGGAGCCCGAGGATACAGGGGCTGAGAGACAGG 353
 431 yNeaAsnTrpSerCysArgThrProGluProAsnProValThrGlyArg 448
 354 CATGACACGCTCTGACGAGCTCCGAGCCCAATCCACTAACAGAGCAG 403
 448 rOLeUValAsnIleTyrAsnCysSerGlyValGln 459
 404 CGCTGTTAACTATCACTGCTCTGGGGTGCA 438

seq_name: gb-est1:AW106218

seq_documentation_block:

LOCUS AW106218 821 bp mRNA linear EST 20-OCT-1999

DEFINITION um24906.y1 Sugano mouse embryo mewa Mus musculus cDNA clone

IMAGE:2225530 5' similar to TR:0922P5 0922P5 HOMOXYSTRINE

RESPONDENT PROTEIN HCYP2.1, mRNA sequence.

ACCESSION AW106218

VERSION AW106218.1 GI:6076954

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 821)

Marr, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T.,

Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person

, B., Swaller, T., Glibson, M., Pape, D., Harvey, N., Schurk, R., Ritter

, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterson, R., and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Other_ESTs: um24906.x1

Contact: Maira M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouse@lewisson.wustl.edu

This clone is available royalty-free through LUML; contact the


```

100 lysSerLeuSerGlyLeuLeuGlnSerGlnCysProAlaArgProIleProLeu 116
101 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
102 GCCTCCCTCCAGAGCGCTGTCGAACCCGAGTCCCTCCGCGCCCTCCGCGCACC 152
117 LeuGlyArgLeuLeuGlyGluValValLeuGlnMetPheTyrLeuHisAs 133
118 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
119 CTCTGTCGCGCTGCTGCAGAGAGTGGTGGGAGATGCTCTACCTACACAG 202
133 pcGlnAspProValLeuLeuHisArgAspLeuLysProSerAsnValLeuP 150
134 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
135 CTGGAACCCCTCCGCTCTCCACCGGAGCTCAAGCCCTTCAACATTTCTGC 252
150 roAspProGluLeuHisValLysLeuAlaAspPheGlyLeuSerThrPhe 166
151 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
152 TGCATCCAGAGCTCCACCCCAAGCTACAGCATTTTTCGCTCCACCTTT 302
167 GlnGlyGlySerGlnSerGlyThrGlySerGly.....GluP 179
168 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
169 CAGGAGAGGTCCTCCAGTCAGGATCAGATCAGATCAGATCAGAGGACCTC 352
179 OGlyGlyThrLeuGlyTyrLeuAlaProGluLeuPheValAsnValAsn 196
180 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 TGGGGGACCCCTAGCCTACTGACCCAGACCTGTTATTTGATGATCAACC 402
196 rglYsAlaSerThrAlaSerAspValTyrSerPheGlyIleLeuMetTrp 212
197 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
198 TGAAGGCTTCTMAAGCGAGTGAATGCTACACCTTTGGATCGCTGCTGG 432
213 AlaValLeuAlaGlyArgGlyValGluLeuProThrGlnProSerLeu 229
214 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
215 GCAGTCTGCTGCTGCAGAGACAGTGAAGTTGGTAGACAGACCTTCACTAA 502
229 aLTrpGluAlaValLysAsnArgGlnAsnArgProSerLeuAlaGluLeu 245
230 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
231 TCCGGGAAACAGCTGTCTCAGAGCAGAGTCTCTCCACCTGACAGACCTG 552
246 ProGlnAlaGlyProGluThrProGlyLeuGlnGlyLeuLysGluLeu 261
247 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
253 CCCTCCAGTAGAGCCCTGAGACTCCCGCTTGGAAGAACTGAAGAGATTA 600
seq_name: gb_ests:B1413255

seq documentation block:
LOCUS B1413255 860 bp mRNA linear EST 14-AUG-2001
DEFINITION 602986355F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142718 5',
mRNA sequence.
ACCESSION B1413255
VERSION B1413255.1 GI:15174178
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 860)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/,
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
plate: L14M11351 row: m column: 23
High quality sequence start: 25
High quality sequence stop: 727.
Location/Qualifiers
1..860
/organism="Mus musculus"

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/strain="C28H 11"
/db_xref="taxon:10090"
/clone="IMAGE:5142718"
/clone_11b="NCI_CGAP_Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/mole="Organ: lung; Vector: pTZ19-Pac (Pharmacia) with a
modified polylinker: Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer 15'.
TestACCAATCTCAAGTGGAGGCGGCGGCTCTCTTTTCTTTTCTTTT 3'1.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTZ19 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 187 a 232 c 247 g 194 t
ORIGIN

alignment_scores:
Quality: 690.50 Length: 223
Ratio: 3.794 Gaps: 6
Percent Similarity: 81.614 Percent Identity: 67.713

alignment block:
US-09-762-491-6 x B1413255 ..
Align seg 1/1 to: B1413255 from: 1 to: 860

1 MetSerCysValLysLeuTrpProSerGlyAlaProAla...ProLeuVal 16
141 ATGCTTTCTGTCAGATTATGCTTACCTGCTGCTCAGCCCTCTCCGCT 190
16 lserIleGlnGluLeuGlnAsnGlnLeuValGlyLysAspGlyPheG 33
191 GAGCGGTGAAGAACTGAAGAACTGAGTTGTGTGGCCAAAGGAGGCTTG 240
33 lYThrValPheATGAlaGlnHisArgLysTrpGlyTyrAspValAlaVal 49
241 GAGTCTGTTTCCGGGCGCACACAGAACATGAACTGATGATGAGCAGTC 290
50 lYsIleValAsnSerLysAlaIleSerArgGluValLysAlaMetLase 66
291 AAGATCGTGAAGCTGGAAGAAATCTGGGAGGCTGAAGTGGTAA 340
66 rLeuAspAsnGluPheValLeuArgLeuGlnGlyValIleGluLysValA 83
341 TCTTCGTAATGAGAACGTTCTGCTGCTGCTGGGGATCATGAGGACCTCC 390
83 aNTrpAspGlnAspProLysProAlaIleuValThrLysPheMetGluAsn 99
391 AOTGGAGATTCGTGTCGCGGACGCTCTGTGACAACTTCAATGAGAAAT 440
100 GlySerLeuSerGlyLeuLeuGlnSerGlnCysProAlaArgProIlePro 116
441 GGTCTCCCTCCAGAGGCTGCTGCAACCAAGATGCTCCGCGCTGCGCACT 490
116 lLeuGlyArgLeuLeuGlyGluValValLeuGlnMetPheTyrLeuHis 133
491 CCTCTGTCGCGCTGCTGCAGAGATGCTCTGCGCATGCTCTACCTACACA 540
133 spGlnAspProValLeuLeuHisArgAspLeuLysProSerAsnValLe 149
541 GCTTGGAGACCTCCGCTCTGCAACCGGAGCTCAAGACCTCTTAACTTC 590
149 uPAspProGluLeuHisValLysLeuAlaAspPheGlyLeuSerThrP 166
591 GCTGATCCAGAGCTCCACGCCAAGCTAGCAATTTGGCTGCTCCACCT 640
166 hc GlnGlyGlySerGlnSerGlyThrGlySerGly.....Glu 178
641 ATTCAGGAGAGGTCCTCCAGTCAAGGATCAGATCAGATCAGATCAGGCA 690

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